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**Figure 1: 158P1D7 SSH sequence (SEQ ID NO: 1).**

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1  GATCTGATAA GCTTTCAATG TTGCGCTCCT GACAATGTAT TAGAAGTCCT GATGGGGATA
61 GGACTTTGCA GTTACAAGGA ATAGGGCAGA AAGGTCCTGG AAGTTGAGTG GATGGCTTTG
121 TAATATAAGG TATCAAACCT GGTGCTTTGG TGGGTAGTTT TAGAATGGAC GTGGTCTTAG
181 TTGACATGCG ACTATCATT ATTGAAGATG TTGCTGCCAG ATGTAATGAT C
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Figure 2:

Figure 2A. The cDNA (SEQ ID NO: 2) and amino acid sequence (SEQ ID NO: 3) of 158P1D7 v.1.

The start methionine is underlined. The open reading frame extends from nucleic acid 23-2548 including the stop codon.

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1           M K L W I H L F Y S S L L
1 t c g g a t t t c a t c a c a t g a c a a c A T G A A G C T G T G G A T T C A T C T C T T T A T T C A T C T C T C C T
14 A C I S L H S Q T P V L S S R G S C D S
61 T G C C T G T A T A T C T T T A C A C T C C C A A A C T C C A G T G C T C T C A T C C A G A G G C T C T T G T G A T T C
34 L C N C E E K D G T M L I N C E A K G I
121 T C T T T G C A A T T G T G A G G A A A A G A T G G C A C A A T G C T A A T A A A T T G T G A A G C A A A A G G T A T
54 K M V S E I S V P P S R P F Q L S L L N
181 C A A G A T G G T A T C T G A A A T A A G T G T G C C A C C A T C A C G A C C T T T C C A A C T A A G C T T A T T A A A
74 N G L T M L H T N D F S G L T N A I S I
241 T A A C G G C T T G A C G A T G C T T C A C A C A A A T G A C T T T T C T G G G C T T A C C A A T G C T A T T T C A A T
94 H L G F N N I A D I E I G A F N G L G L
301 A C A C C T T G G A T T T A A C A A T A T T G C A G A T A T T G A G A T A G G T G C A T T T A A T G G C C T T G G C C T
114 L K Q L H I N H N S L E I L K E D T F H
361 C C T G A A C A A C T T C A T A T C A A T C A C A A T T C T T T A G A A A T T C T T A A G A G G A T A C T T T C C A
134 G L E N L E F L Q A D N N F I T V I E P
421 T G G A C T G G A A A C C T G G A A T T C C T G C A A G C A G A T A A C A A T T T T A T C A C A G T G A T T G A A C C
154 S A F S K L N R L K V L I L N D N A I E
481 A A G T G C C T T T A G C A A G C T C A A C A G A C T C A A A G T G T T A A T T T T A A A T G A C A A T G C T A T T G A
174 S L P P N I F R F V P L T H L D L R G N
541 G A G T C T T C C T C C A A A C A T C T T C C G A T T T G T T C C T T T A A C C A T C T A G A T C T T C G T G G A A A
194 Q L Q T L P Y V G F L E H I G R I L D L
601 T C A A T T A C A A C A T T G C C T T A T G T T G G T T T T C T C G A A C A C A T T G G C C G A A T A T T G G A T C T
214 Q L E D N K W A C N C D L L Q L K T W L
661 T C A G T T G G A G G A C A A C A A A T G G G C C T G C A A T T G T G A C T T A T T G C A G T T A A A A C T T G G T T
234 E N M P P Q S I I G D V V C N S P P F F
721 G G A G A A C A T G C C T C C A C A G T C T A T A A T T G G T G A T G T T G T C T G C A A C A G C C C T C C A T T T T T
254 K G S I L S R L K K E S I C P T P P V Y
781 T A A A G G A A G T A T A C T C A G T A G A C T A A A G A A G G A A T C T A T T T G C C C T A C T C C A C C A G T G T A
274 E E H E D P S G S L H L A A T S S I N D
841 T G A A G A A C A T G A G G A T C C T T C A G G A T C A T T A C A T C T G G C A G C A A C A T C T T C A A T A A A T G A
294 S R M S T K T T S I L K L P T K A P G L
901 T A G T C G C A T G T C A A C T A A G A C C A C G T C C A T T C T A A A A C T A C C C A C C A A A G C A C C A G G T T T
314 I P Y I T K P S T Q L P G P Y C P I P C
961 G A T A C C T T A T A T T A C A A A G C C A T C C A C T C A A C T T C C A G G A C C T T A C T G C C C T A T T C C T T G
334 N C K V L S P S G L L I H C Q E R N I E
1021 T A A C T G C A A A G T C C T A T C C C C A T C A G G A C T T C T A A T A C A T T G T C A G G A G C G C A A C A T T G A
354 S L S D L R P P P Q N P R K L I L A G N

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1081 AAGCTTATCAGATCTGAGACCTCCTCCGCAAAATCCTAGAAAGCTCATTCTAGCGGAAAA  
374 I I H S L M K S D L V E Y F T L E M L H  
1141 TATTATTCACAGTTTAATGAAGTCTGATCTAGTGAATATTTCACTTTGGAAATGCTTCA  
394 L G N N R I E V L E E G S F M N L T R L  
1201 CTTGGGAAACAATCGTATTGAAGTTCTTGAAGAAGGATCGTTTATGAACCTAACGAGATT  
414 Q K L Y L N G N H L T K L S K G M F L G  
1261 ACAAAAACCTCTATCTAAATGGTAACCACCTGACCAAATTAAGTAAAGGCATGTTCTTGG  
434 L H N L E Y L Y L E Y N A I K E I L P G  
1321 TCTCCATAATCTTGAATACTTATATCTTGAATACAATGCCATTAAGGAAATACTGCCAGG  
454 T F N P M P K L K V L Y L N N N L L Q V  
1381 AACCTTTAATCCAATGCCTAACTTAAAGTCCTGTATTTAAATAACAACCTCCTCCAAGT  
474 L P P H I F S G V P L T K V N L K T N Q  
1441 TTTACCACCACATATTTTTTTCAGGGGTTCTCTAACTAAGGTAAATCTTAAAACAAACCA  
494 F T H L P V S N I L D D L D L L T Q I D  
1501 GTTTACCCATCTACCTGTAAGTAATATTTTGGATGATCTTGATTACTAACCCAGATTGA  
514 L E D N P W D C S C D L V G L Q Q W I Q  
1561 CCTTGAGGATAACCCCTGGGACTGCTCCTGTGACCTGGTTGGACTGCAGCAATGGATACA  
534 K L S K N T V T D D I L C T S P G H L D  
1621 AAAGTTAAGCAAGAACACAGTGACAGATGACATCCTCTGCACTTCCCCCGGCATCTCGA  
554 K K E L K A L N S E I L C P G L V N N P  
1681 CAAAAAGGAATTGAAAGCCCTAAATAGTGAAATTCTCTGTCCAGGTTTAGTAAATAACCC  
574 S M P T Q T S Y L M V T T P A T T T N T  
1741 ATCCATGCCAACACAGACTAGTTACCTTATGGTCACCACTCCTGCAACAACAACAAATAC  
594 A D T I L R S L T D A V P L S V L I L G  
1801 GGCTGATACTATTTTACGATCTCTTACGGACGCTGTGCCACTGTCTGTTCTAATATTGGG  
614 L L I M F I T I V F C A A G I V V L V L  
1861 ACTTCTGATTATGTTTCATCACTATTGTTTCTGTGCTGCAGGGATAGTGGTTCTTGTTC  
634 H R R R R Y K K K Q V D E Q M R D N S P  
1921 TCACCGCAGGAGAAGATACAAAAAGAAACAAGTAGATGAGCAAATGAGAGACAACAGTCC  
654 V H L Q Y S M Y G H K T T H H T T E R P  
1981 TGTGCATCTTCAGTACAGCATGTATGGCCATAAAACCACTCATCACTACTGAAAGACC  
674 S A S L Y E Q H M V S P M V H V Y R S P  
2041 CTCTGCCTCACTCTATGAACAGCACATGGTGAGCCCCATGGTTCATGTCTATAGAAGTCC  
694 S F G P K H L E E E E E R N E K E G S D  
2101 ATCCTTTGGTCCAAAGCATCTGGAAGAGGAAGAAGAGAGGAATGAGAAAGAAGGAAGTGA  
714 A K H L Q R S L L E Q E N H S P L T G S  
2161 TGCAAAACATCTCCAAAGAAGTCTTTTGGAAACAGGAAAATCATTCACTACTCACAGGGTC  
734 N M K Y K T T N Q S T E F L S F Q D A S  
2221 AAATATGAAATACAAAACCACGAACCAATCAACAGAATTTTTATCCTTCCAAGATGCCAG  
754 S L Y R N I L E K E R E L Q Q L G I T E  
2281 CTCATTGTACAGAAACATTTTAGAAAAAGAAAGGGAACCTCAGCAACTGGGAATCACAGA  
774 Y L R K N I A Q L Q P D M E A H Y P G A

2341 ATACCTAAGGAAAAACATTGCTCAGCTCCAGCCTGATATGGAGGCACATTATCCTGGAGC  
794 H E E L K L M E T L M Y S R P R K V L V  
2401 CCACGAAGAGCTGAAGTTAATGGAAACATTAATGTACTCACGTCCAAGGAAGGTATTAGT  
814 E Q T K N E Y F E L K A N L H A E P D Y  
2461 GGAACAGACAAAAAATGAGTATTTTGAACCTAAAGCTAATTTACATGCTGAACCTGACTA  
834 L E V L E Q Q T \*  
2521 TTTAGAAGTCCTGGAGCAGCAAACATAGatggaga

**Figure 2B. The cDNA (SEQ ID NO: 4) and amino acid sequence (SEQ ID NO: 5) of 158P1D7 v.2.**  
The start methionine is underlined. The open reading frame extends from nucleic acid 23-2548 including the stop codon.

1 M K L W I H L F Y S S L L  
1 t c g g a t t t c a t c a c a t g a c a a c A T G A A G C T G T G G A T T C A T C T C T T T T A T T C A T C T C T C C T  
14 A C I S L H S Q T P V L S S R G S C D S  
61 T G C C T G T A T A T C T T T A C A C T C C C A A A C T C C A G T G C T C T C A T C C A G A G G C T C T T G T G A T T C  
34 L C N C E E K D G T M L I N C E A K G I  
121 T C T T T G C A A T T G T G A G G A A A A G A T G G C A C A A T G C T A A T A A A T T G T G A A G C A A A A G G T A T  
54 K M V S E I S V P P S R P F Q L S L L N  
181 C A A G A T G G T A T C T G A A A T A A G T G T G C C A C C A T C A C G A C C T T T C C A A C T A A G C T T A T T A A A  
74 N G L T M L H T N D F S G L T N A I S I  
241 T A A C G G C T T G A C G A T G C T T C A C A C A A A T G A C T T T T C T G G G C T T A C C A A T G C T A T T T C A A T  
94 H L G F N N I A D I E I G A F N G L G L  
301 A C A C C T T G G A T T T A A C A A T A T T G C A G A T A T T G A G A T A G G T G C A T T T A A T G G C C T T G G C C T  
114 L K Q L H I N H N S L E I L K E D T F H  
361 C C T G A A C A A C T T C A T A T C A A T C A C A A T T C T T T A G A A A T T C T T A A A G A G G A T A C T T T C C A  
134 G L E N L E F L Q A D N N F I T V I E P  
421 T G G A C T G G A A A C C T G G A A T T C C T G C A A G C A G A T A A C A A T T T T A T C A C A G T G A T T G A A C C  
154 S A F S K L N R L K V L I L N D N A I E  
481 A A G T G C C T T T A G C A A G C T C A A C A G A C T C A A A G T G T T A A T T T T A A T G A C A A T G C T A T T G A  
174 S L P P N I F R F V P L T H L D L R G N  
541 G A G T C T T C C T C C A A C A T C T T C C G A T T T G T T C C T T T A A C C C A T C T A G A T C T T C G T G G A A A  
194 Q L Q T L P Y V G F L E H I G R I L D L  
601 T C A A T T A C A A C A T T G C C T T A T G T T G G T T T T C T C G A A C A C A T T G G C C G A A T A T T G G A T C T  
214 Q L E D N K W A C N C D L L Q L K T W L  
661 T C A G T T G G A G G A C A C A A A T G G G C C T G C A A T T G T G A C T T A T T G C A G T T A A A A C T T G G T T  
234 E N M P P Q S I I G D V V C N S P P F F  
721 G G A G A A C A T G C C T C C A C A G T C T A T A A T T G G T G A T G T T G T C T G C A A C A G C C C T C C A T T T T T  
254 K G S I L S R L K K E S I C P T P P V Y  
781 T A A A G G A A G T A T A C T C A G T A G A C T A A A G A A G G A A T C T A T T T G C C C T A C T C C A C C A G T G T A  
274 E E H E D P S G S L H L A A T S S I N D  
841 T G A A G A C A T G A G G A T C C T T C A G G A T C A T T A C A T C T G G C A G C A A C A T C T T C A A T A A A T G A

294 S R M S T K T T S I L K L P T K A P G L  
901 TAGTCGCATGTCAACTAAGACCACGTCCATTCTAAAACTACCCACCAAAGCACCAGGTTT  
314 I P Y I T K P S T Q L P G P Y C P I P C  
961 GATACCTTATATTACAAAGCCATCCACTCAACTTCCAGGACCTTACTGCCCTATTCTTGG  
334 N C K V L S P S G L L I H C Q E R N I E  
1021 TAACTGCAAAGTCCTATCCCCATCAGGACTTCTAATACATTGTCAGGAGCGCAACATTGA  
354 S L S D L R P P P Q N P R K L I L A G N  
1081 AAGCTTATCAGATCTGAGACCTCCTCCGCAAAATCCTAGAAAGCTCATTCTAGCGGGAAA  
374 I I H S L M K S D L V E Y F T L E M L H  
1141 TATTATTCACAGTTTAATGAAGTCTGATCTAGTGAATATTTCACTTTGGAAATGCTTCA  
394 L G N N R I E V L E E G S F M N L T R L  
1201 CTTGGGAAACAATCGTATTGAAGTTCTTGAAGAAGGATCGTTTATGAACCTAACGAGATT  
414 Q K L Y L N G N H L T K L S K G M F L G  
1261 ACAAAAACCTCTATCTAAATGGTAACCACCTGACCAAATTAAGTAAAGGCATGTTCTTGG  
434 L H N L E Y L Y L E Y N A I K E I L P G  
1321 TCTCCATAATCTTGAATACTTATATCTTGAATACAATGCCATTAAGGAAATACTGCCAGG  
454 T F N P M P K L K V L Y L N N N L L Q V  
1381 AACCTTTAATCCAATGCCTAAACTTAAAGTCTGTATTTAAATAACAACCTCCTCCAAGT  
474 L P P H I F S G V P L T K V N L K T N Q  
1441 TTTACCACCACATATTTTTTTCAGGGGTTCTCTAACTAAGGTAAATCTTAAACAAACCA  
494 F T H L P V S N I L D D L D L L T Q I D  
1501 GTTTACCCATCTACCTGTAAGTAATATTTTGGATGATCTTGATTGCTAACCCAGATTGA  
514 L E D N P W D C S C D L V G L Q Q W I Q  
1561 CCTTGAGGATAACCCCTGGGACTGCTCCTGTGACCTGGTTGGACTGCAGCAATGGATACA  
534 K L S K N T V T D D I L C T S P G H L D  
1621 AAAGTTAAGCAAGAACACAGTGACAGATGACATCCTCTGCACTTCCCCCGGCATCTCGA  
554 K K E L K A L N S E I L C P G L V N N P  
1681 CAAAAGGAATTGAAAGCCCTAAATAGTGAAATTCTCTGTCCAGGTTTAGTAAATAACCC  
574 S M P T Q T S Y L M V T T P A T T T N T  
1741 ATCCATGCCAACACAGACTAGTTACCTTATGGTCACCACTCCTGCAACAACAACAATAC  
594 A D T I L R S L T D A V P L S V L I L G  
1801 GGCTGATACTATTTTACGATCTCTTACGGACGCTGTGCCACTGTCTGTTCTAATATTGGG  
614 L L I M F I T I V F C A A G I V V L V L  
1861 ACTTCTGATTATGTTTCATCACTATTGTTTTCTGTGCTGCAGGGATAGTGGTTCTTGTTC  
634 H R R R R Y K K K Q V D E Q M R D N S P  
1921 TCACCGCAGGAGAAGATACAAAAGAAACAAGTAGATGAGCAAATGAGAGACAACAGTCC  
654 V H L Q Y S M Y G H K T T H H T T E R P  
1981 TGTGCATCTTCAGTACAGCATGTATGGCCATAAAACCACTCATCACTACTGAAAGACC  
674 S A S L Y E Q H M V S P M V H V Y R S P  
2041 CTCTGCCTCACTCTATGAACAGCACATGGTGAGCCCCATGGTTCATGTCTATAGAAGTCC  
694 S F G P K H L E E E E E R N E K E G S D  
2101 ATCCTTTGGTCCAAAGCATCTGGAAGAGGAAGAAGAGAGGAATGAGAAAGAAGGAAGTGA

714 A K H L Q R S L L E Q E N H S P L T G S  
2161 TGCAAAACATCTCCAAAGAAGTCTTTTGAACAGGAAAATCATTACCACTCACAGGGTC  
734 N M K Y K T T N Q S T E F L S F Q D A S  
2221 AAATATGAAATACAAAACCACGAACCAATCAACAGAATTTTATCCTTCCAAGATGCCAG  
754 S L Y R N I L E K E R E L Q Q L G I T E  
2281 CTCATTGTACAGAAACATTTTAGAAAAAGAAAGGGAACCTCAGCAACTGGGAATCACAGA  
774 Y L R K N I A Q L Q P D M E A H Y P G A  
2341 ATACCTAAGGAAAAACATTGCTCAGCTCCAGCCTGATATGGAGGCACATTATCCTGGAGC  
794 H E E L K L M E T L M Y S R P R K V L V  
2401 CCACGAAGAGCTGAAGTTAATGGAAACATTAATGTACTCACGTCCAAGGAAGGTATTAGT  
814 E Q T K N E Y F E L K A N L H A E P D Y  
2461 GGAACAGACAAAAAATGAGTATTTGAACTTAAAGCTAATTTACATGCTGAACCTGACTA  
834 L E V L E Q Q T \*  
2521 TTTAGAAGTCCTGGAGCAGCAAACATAGatggaga

**Figure 2C. The cDNA (SEQ ID NO: 6) and amino acid sequence (SEQ ID NO: 7) of 158P1D7 v.3.**  
The start methionine is underlined. The open reading frame extends from nucleic acid 23-2221 including the stop codon.

1 M K L W I H L F Y S S L L  
1 tcggatttcacatgacaacATGAAGCTGTGGATTCATCTCTTTTATTCATCTCTCCT  
14 A C I S L H S Q T P V L S S R G S C D S  
61 TGCCTGTATATCTTTACACTCCCAAACCTCCAGTGCTCTCATCCAGAGGCTCTTGTGATTC  
34 L C N C E E K D G T M L I N C E A K G I  
121 TCTTTGCAATTGTGAGGAAAAAGATGGCACAATGCTAATAAATTGTGAAGCAAAAGGTAT  
54 K M V S E I S V P P S R P F Q L S L L N  
181 CAAGATGGTATCTGAAATAAGTGTGCCACCATCACGACCTTTCCAACCTAAGCTTATTAAA  
74 N G L T M L H T N D F S G L T N A I S I  
241 TAACGGCTTGACGATGCTTCACACAAATGACTTTTCTGGGCTTACCAATGCTATTTCAAT  
94 H L G F N N I A D I E I G A F N G L G L  
301 ACACCTTGGATTTAACAATATTGCAGATATTGAGATAGGTGCATTTAATGGCCTTGGCCT  
114 L K Q L H I N H N S L E I L K E D T F H  
361 CCTGAAACAACTTCATATCAATCACAATTCTTTAGAAATTCTTAAAGAGGATACTTTCCA  
134 G L E N L E F L Q A D N N F I T V I E P  
421 TGGACTGGAAAACCTGGAATTCCTGCAAGCAGATAACAATTTTATCACAGTGATTGAACC  
154 S A F S K L N R L K V L I L N D N A I E  
481 AAGTGCCTTTAGCAAGCTCAACAGACTCAAAGTGTTAATTTTAAATGACAATGCTATTGA  
174 S L P P N I F R F V P L T H L D L R G N  
541 GAGTCTTCCTCCAAACATCTTCCGATTTGTTCTTTAACCCATCTAGATCTTCGTGGAAA  
194 Q L Q T L P Y V G F L E H I G R I L D L  
601 TCAATTACAAACATTGCCTTATGTTGGTTTCTCGAACACATTGGCCGAATATTGGATCT  
214 Q L E D N K W A C N C D L L Q L K T W L

661 TCAGTTGGAGGACAACAAATGGGCCTGCAATTGTGACTTATTGCAGTTAAAACTTGGTT  
234 E N M P P Q S I I G D V V C N S P P F F  
721 GGAGAACATGCCTCCACAGTCTATAATTGGTGATGTTGTCTGCAACAGCCCTCCATTTTT  
254 K G S I L S R L K K E S I C P T P P V Y  
781 TAAAGGAAGTATACTCAGTAGACTAAAGAAGGAATCTATTTGCCCTACTCCACCAGTGTA  
274 E E H E D P S G S L H L A A T S S I N D  
841 TGAAGACATGAGGATCCTTCAGGATCATTACATCTGGCAGCAACATCTTCAATAAATGA  
294 S R M S T K T T S I L K L P T K A P G L  
901 TAGTCGCATGTCAACTAAGACCACGTCCATTCTAAAACTACCCACCAAAGCACCAGTTT  
314 I P Y I T K P S T Q L P G P Y C P I P C  
961 GATACCTTATATTACAAAGCCATCCACTCAACTTCCAGGACCTTACTGCCCTATTTCCTTG  
334 N C K V L S P S G L L I H C Q E R N I E  
1021 TAACTGCAAAGTCCTATCCCCATCAGGACTTCTAATACATTGTCAGGAGCGCAACATTGA  
354 S L S D L R P P P Q N P R K L I L A G N  
1081 AAGCTTATCAGATCTGAGACCTCCTCCGAAAATCCTAGAAAGCTCATTCTAGCGGGAAA  
374 I I H S L M K S D L V E Y F T L E M L H  
1141 TATTATTCACAGTTTAATGAAGTCTGATCTAGTGGAATATTTCACTTTGGAAATGCTTCA  
394 L G N N R I E V L E E G S F M N L T R L  
1201 CTTGGGAAACAATCGTATTGAAGTTCTTGAAGAAGGATCGTTTATGAACCTAACGAGATT  
414 Q K L Y L N G N H L T K L S K G M F L G  
1261 ACAAAAACCTCTATCTAAATGGTAACCACCTGACCAAATTAAGTAAAGGCATGTTCTCTGG  
434 L H N L E Y L Y L E Y N A I K E I L P G  
1321 TCTCCATAATCTTGAATACTTATATCTTGAATACAATGCCATTAAGGAAATACTGCCAGG  
454 T F N P M P K L K V L Y L N N N L L Q V  
1381 AACCTTTAATCCAATGCCTAAACTTAAAGTCCTGTATTTAAATAACAACCTCCTCCAAGT  
474 L P P H I F S G V P L T K V N L K T N Q  
1441 TTTACCACCACATATTTTTTTCAGGGGTTCTCTAACTAAGGTAAATCTTAAAACAAACCA  
494 F T H L P V S N I L D D L D L L T Q I D  
1501 GTTTACCCATCTACCTGTAAGTAATATTTTGGATGATCTTGATTTACTAACCAGATTGA  
514 L E D N P W D C S C D L V G L Q Q W I Q  
1561 CCTTGAGGATAACCCCTGGGACTGCTCCTGTGACCTGGTTGGACTGCAGCAATGGATACA  
534 K L S K N T V T D D I L C T S P G H L D  
1621 AAAGTTAAGCAAGAACACAGTGACAGATGACATCCTCTGCACTTCCCCGGGCATCTCGA  
554 K K E L K A L N S E I L C P G L V N N P  
1681 CAAAAAGGAATTGAAAGCCCTAAATAGTGAAATTCTCTGTCCAGGTTTAGTAAATAACCC  
574 S M P T Q T S Y L M V T T P A T T T N T  
1741 ATCCATGCCAACACAGACTAGTTACCTTATGGTCACCACTCCTGCAACAACAACAAATAC  
594 A D T I L R S L T D A V P L S V L I L G  
1801 GGCTGATACTATTTTACGATCTCTTACGGACGCTGTGCCACTGTCTGTTCTAATATTGGG  
614 L L I M F I T I V F C A A G I V V L V L  
1861 ACTTCTGATTATGTTTCATCACTATTGTTTTCTGTGCTGCAGGGATAGTGGTTCTTGTTC  
634 H R R R R Y K K K Q V D E Q M R D N S P



1921 TCACCGCAGGAGAAGATACAAAAAGAAACAAGTAGATGAGCAAATGAGAGACAACAGTCC  
654 V H L Q Y S M Y G H K T T H H T T E R P  
1981 TGTGCATCTTCAGTACAGCATGTATGGCCATAAAACCACTCATCAGTACTGAAAGACC  
674 S A S L Y E Q H M G A H E E L K L M E T  
2041 CTCTGCCTCACTCTATGAACAGCACATGGGAGCCCACGAAGAGCTGAAGTTAATGGAAAC  
694 L M Y S R P R K V L V E Q T K N E Y F E  
2101 ATTAATGTACTCAGTCCAAGGAAGGTATTAGTGGAACAGACAAAAATGAGTATTTTGA  
714 L K A N L H A E P D Y L E V L E Q Q T \*  
2161 ACTTAAAGCTAATTTACATGCTGAACCTGACTATTTAGAAGTCTCTGGAGCAGCAAACATA  
2221 Gatggaga

**Figure 2D. The cDNA (SEQ ID NO: 8) and amino acid sequence (SEQ ID NO: 9) of 158P1D7 v.4.**

The start methionine is underlined. The open reading frame extends from nucleic acid 23-1210 including the stop codon.

1 M K L W I H L F Y S S L L  
1 tcggatttcatcacatgacaacATGAAGCTGTGGATTCATCTCTTTATTCATCTCTCCT  
14 A C I S L H S Q T P V L S S R G S C D S  
61 TGCCTGTATATCTTTACTCCAACTCCAGTGCTCTCATCCAGAGGCTCTTGTGATT  
34 L C N C E E K D G T M L I N C E A K G I  
121 TCTTTGCAATTGTGAGGAAAAAGATGGCACAATGCTAATAAATTGTGAAGCAAAGGTAT  
54 K M V S E I S V P P S R P F Q L S L L N  
181 CAAGATGGTATCTGAAATAAGTGTGCCACCATCACGACCTTTCCAACTAAGCTTATTAA  
74 N G L T M L H T N D F S G L T N A I S I  
241 TAACGGCTTGACGATGCTTCACACAAATGACTTTTCTGGGCTTACCAATGCTATTTCAAT  
94 H L G F N N I A D I E I G A F N G L G L  
301 ACACCTTGGATTTAACAATATTGCAGATATTGAGATAGGTGCATTAAATGGCCTTGGCCT  
114 L K Q L H I N H N S L E I L K E D T F H  
361 CCTGAAACAACTTCATATCAATCACAATTCTTTAGAAATTCTTAAAGAGGATACTTTCCA  
134 G L E N L E F L Q A D N N F I T V I E P  
421 TGGACTGGAAAACCTGGAATTCCTGCAAGCAGATAACAATTTTATCACAGTGATTGAACC  
154 S A F S K L N R L K V L I L N D N A I E  
481 AAGTGCCTTTAGCAAGCTCAACAGACTCAAAGTGTTAATTTTAAATGACAATGCTATTGA  
174 S L P P N I F R F V P L T H L D L R G N  
541 GAGTCTTCCTCCAAACATCTTCCGATTGTTCCTTTAACCCATCTAGATCTTCGTGGAAA  
194 Q L Q T L P Y V G F L E H I G R I L D L  
601 TCAATTACAAACATTGCCTTATGTTGGTTTCTCGAACACATTGGCCGAATATTGGATCT  
214 Q L E D N K W A C N C D L L Q L K T W L  
661 TCAGTTGGAGGACAACAAATGGGCCTGCAATTGTGACTTATTGCAGTTAAAACTTGGTT  
234 E N M P P Q S I I G D V V C N S P P F F  
721 GGAGAACATGCCTCCACAGTCTATAATTGGTGATGTTGTCTGCAACAGCCCTCCATTTT  
254 K G S I L S R L K K E S I C P T P P V Y

781 TAAAGGAAGTATACTCAGTAGACTAAAGAAGGAATCTATTTGCCCTACTCCACCAGTGTA  
274 E E H E D P S G S L H L A A T S S I N D  
841 TGAAGAACATGAGGATCCTTCAGGATCATTACATCTGGCAGCAACATCTTCAATAAATGA  
294 S R M S T K T T S I L K L P T K A P G L  
901 TAGTCGCATGTCAACTAAGACCACGTCCATTCTAAAACTACCCACCAAAGCACCAGGTTT  
314 I P Y I T K P S T Q L P G P Y C P I P C  
961 GATACCTTATATTACAAAGCCATCCACTCAACTTCCAGGACCTTACTGCCCTATTCTTTG  
334 N C K V L S P S G L L I H C Q E R N I E  
1021 TAACTGCAAAGTCTATCCCCATCAGGACTTCTAATACATTGTCAGGAGCGCAACATTGA  
354 S L S D L R P P P Q N P R K L I L A G N  
1081 AAGCTTATCAGATCTGAGACCTCCTCCGCAAAATCCTAGAAAGCTCATTCTAGCGGGAAA  
374 I I H S L M K S I L W S K A S G R G R R  
1141 TATTATTCACAGTTTAATGAAGTCCATCCTTTGGTCCAAAGCATCTGGAAGAGGAAGAAG  
394 E E \*  
1201 AGAGGAATGAgaaagaaggaagtgatgcaaaacatctccaaagaagtcttttggaaacagg  
1261 aaaatcattcaccactcacagggtcaaatatgaaatacaaaaccacgaaccaatcaacag  
1321 aatttttatccttccaagatgccagctcattgtacagaaacattttagaaaaagaaaggg  
1381 aacttcagcaactgggaatcacagaatacctaaggaaaaacattgctcagctccagcctg  
1441 atatggaggcacattatcctggagcccacgaagagctgaagttaatggaaacattaatgt  
1501 actcacgtccaaggaaggtattagtggaacagacaaaaaatgagtattttgaacttaaag  
1561 ctaatttacatgctgaacctgactatttagaagtcctggagcagcaaacatagatggaga

**Figure 2E. The cDNA (SEQ ID NO: 10) and amino acid sequence (SEQ ID NO: 11) of 158P1D7 v.5.**  
The start methionine is underlined. The open reading frame extends from nucleic acid 480-3005 including the stop codon.

1 gcgtcgacaacaagaaatactagaaaaggaggaaggagaacattgctgcagcttggatct  
61 acaacctaagaaagcaagagtgatcaatctcagctctgttaaacatcttgtttacttact  
121 gcattcagcagcttgcaaattgggttaactatatgcaaaaaagtcagcatagctgtgaagta  
181 tgccgtgaatttttaattgagggaaaaaggacaattgcttcaggatgctctagtagtcact  
241 ctgcttgaaatattttcaatgaaatgctcagtagtattctatctttgaccagagggttttaact  
301 ttatgaagctatgggacttgacaaaaagtgatatttgagaagaaagtacgcagtggttgg  
361 tgtttttcttttttttaataaaggaattgaattactttgaacacctcttccagctgtgcatt  
1 M  
421 tacagataacgtcaggaagagtcctctgctttacagaatcggatttcacatgacaacA  
2 K L W I H L F Y S S L L A C I S L H S Q  
481 TGAAGCTGTGGATTCATCTCTTTTATTCATCTCTCCTTGCCTGTATATCTTTACTACTCCC  
22 T P V L S S R G S C D S L C N C E E K D  
541 AAACTCCAGTGCTCTCATCCAGAGGCTCTTGTGATTCTCTTTGCAATTGTGAGGAAAAAG  
42 G T M L I N C E A K G I K M V S E I S V  
601 ATGGCACAATGCTAATAAAATTGTGAAGCAAAAGGTATCAAGATGGTATCTGAAATAAGTG  
62 P P S R P F Q L S L L N N G L T M L H T

661 TGCCACCATCACGACCTTTCCAACCTAAGCTTATTAAATAACGGCTTGACGATGCTTCACA  
82 N D F S G L T N A I S I H L G F N N I A  
721 CAAATGACTTTTCTGGGCTTACCAATGCTATTTCAATACACCTTGGATTAAACAATATTG  
102 D I E I G A F N G L G L L K Q L H I N H  
781 CAGATATTGAGATAGGTGCATTTAATGGCCTTGGCCTCCTGAAACAACTTCATATCAATC  
122 N S L E I L K E D T F H G L E N L E F L  
841 ACAATTCTTTAGAAATTCTTAAAGAGGATACTTTCCATGGACTGGAAAACCTGGAATTCC  
142 Q A D N N F I T V I E P S A F S K L N R  
901 TGCAAGCAGATAACAATTTTATCACAGTGATTGAACCAAGTGCCTTTAGCAAGCTCAACA  
162 L K V L I L N D N A I E S L P P N I F R  
961 GACTCAAAGTGTTAATTTTAAATGACAATGCTATTGAGAGTCTTCTCCAAACATCTTCC  
182 F V P L T H L D L R G N Q L Q T L P Y V  
1021 GATTTGTTCTTTAACCCATCTAGATCTTCGTGGAAATCAATTACAAACATTGCCTTATG  
202 G F L E H I G R I L D L Q L E D N K W A  
1081 TTGGTTTTCTCGAACACATTGGCCGAATATTGGATCTTCAGTTGGAGGACAACAAATGGG  
222 C N C D L L Q L K T W L E N M P P Q S I  
1141 CCTGCAATTGTGACTTATTGCAGTTAAAACTTGGTTGGAGAACATGCCTCCACAGTCTA  
242 I G D V V C N S P P F F K G S I L S R L  
1201 TAATTGGTGATGTTGTCTGCAACAGCCCTCCATTTTTTAAAGGAAGTATACTCAGTAGAC  
262 K K E S I C P T P P V Y E E H E D P S G  
1261 TAAAGAAGGAATCTATTTGCCCTACTCCACCAGTGTATGAAGAACATGAGGATCCTTCAG  
282 S L H L A A T S S I N D S R M S T K T T  
1321 GATCATTACATCTGGCAGCAACATCTTCAATAAATGATAGTCGCATGTCAACTAAGACCA  
302 S I L K L P T K A P G L I P Y I T K P S  
1381 CGTCCATTCTAAAACTACCCACCAAAGCACCAGGTTTGATACCTTATATTACAAAGCCAT  
322 T Q L P G P Y C P I P C N C K V L S P S  
1441 CCACTCAACTTCCAGGACCTTACTGCCCTATTCCTTGTAAGTCAAAGTCTATCCCCAT  
342 G L L I H C Q E R N I E S L S D L R P P  
1501 CAGGACTTCTAATACATTGTCAGGAGCGCAACATTGAAAGCTTATCAGATCTGAGACCTC  
362 P Q N P R K L I L A G N I I H S L M K S  
1561 CTCCGCAAAATCCTAGAAAGCTCATTCTAGCGGAAATATTATTACAGTTTAAATGAAGT  
382 D L V E Y F T L E M L H L G N N R I E V  
1621 CTGATCTAGTGAATATTTCACTTTGGAAATGCTTCACTTGGGAAACAATCGTATTGAAG  
402 L E E G S F M N L T R L Q K L Y L N G N  
1681 TTCTTGAAGAAGGATCGTTTATGAACCTAACGAGATTACAAAACTCTATCTAAATGGTA  
422 H L T K L S K G M F L G L H N L E Y L Y  
1741 ACCACCTGACCAAATTAAGTAAAGGCATGTTCTTGGTCTCCATAATCTTGAATACTTAT  
442 L E Y N A I K E I L P G T F N P M P K L  
1801 ATCTTGAATACAATGCCATTAAGGAAATACTGCCAGGAACCTTTAATCCAATGCCTAAAC  
462 K V L Y L N N N L L Q V L P P H I F S G  
1861 TTAAAGTCCTGTATTTAAATAACAACCTCCTCCAAGTTTTACCACCACATATTTTTTTCAG  
482 V P L T K V N L K T N Q F T H L P V S N

1921 GGGTTCCTCTAACTAAGGTAAATCTTAAAAACAAACCAGTTTACCCATCTACCTGTAAGTA  
502 I L D D L D L L T Q I D L E D N P W D C  
1981 ATATTTTGGATGATCTTGATTTACTAACCAGATTGACCTTGAGGATAACCCCTGGGACT  
522 S C D L V G L Q Q W I Q K L S K N T V T  
2041 GCTCCTGTGACCTGGTTGGACTGCAGCAATGGATACAAAAGTTAAGCAAGAACACAGTGA  
542 D D I L C T S P G H L D K K E L K A L N  
2101 CAGATGACATCCTCTGCACTTCCCCCGGCATCTCGACAAAAAGGAATTGAAAGCCCTAA  
562 S E I L C P G L V N N P S M P T Q T S Y  
2161 ATAGTGAAATTCTCTGTCCAGGTTTAGTAAATAACCCATCCATGCCAACACAGACTAGTT  
582 L M V T T P A T T T N T A D T I L R S L  
2221 ACCTTATGGTCACCACTCCTGCAACAACAACAAATACGGCTGATACTATTTTACGATCTC  
602 T D A V P L S V L I L G L L I M F I T I  
2281 TTACGGACGCTGTGCCACTGTCTGTTCTAATATTGGGACTTCTGATTATGTTTCATCACTA  
622 V F C A A G I V V L V L H R R R R Y K K  
2341 TTGTTTTCTGTGCTGCAGGGATAGTGGTCTTGTTCCTTACCAGCAGGAGAAGATACAAAA  
642 K Q V D E Q M R D N S P V H L Q Y S M Y  
2401 AGAAACAAGTAGATGAGCAAATGAGAGACAACAGTCCTGTGCATCTTCAGTACAGCATGT  
662 G H K T T H H T T E R P S A S L Y E Q H  
2461 ATGGCCATAAAACCACTCATCACTACTGAAAGACCCTCTGCCTCACTCTATGAACAGC  
682 M V S P M V H V Y R S P S F G P K H L E  
2521 ACATGGTGAGCCCCATGGTTCATGTCTATAGAAGTCCATCCTTGGTCCAAAGCATCTGG  
702 E E E E R N E K E G S D A K H L Q R S L  
2581 AAGAGGAAGAAGAGAGGAATGAGAAAGAAGGAAGTGATGCAAAACATCTCCAAAGAAGTC  
722 L E Q E N H S P L T G S N M K Y K T T N  
2641 TTTTGGAACAGGAAAATCATTCACTCACTCAGGGTCAAATATGAAATACAAAACCACGA  
742 Q S T E F L S F Q D A S S L Y R N I L E  
2701 ACCAATCAACAGAATTTTTATCCTTCCAAGATGCCAGCTCATTGTACAGAAACATTTTAG  
762 K E R E L Q Q L G I T E Y L R K N I A Q  
2761 AAAAAGAAAGGGAACCTCAGCAACTGGGAATCACAGAATACCTAAGGAAAAACATTGCTC  
782 L Q P D M E A H Y P G A H E E L K L M E  
2821 AGCTCCAGCTGATATGGAGGCACATTATCCTGGAGCCCACGAAGAGCTGAAGTTAATGG  
802 T L M Y S R P R K V L V E Q T K N E Y F  
2881 AAACATTAATGTACTCACGTCCAAGGAAGGTATTAGTGGAACAGACAAAAATGAGTATT  
822 E L K A N L H A E P D Y L E V L E Q Q T  
2941 TTGAACCTAAAGCTAATTTACATGCTGAACCTGACTATTTAGAAGTCCTGGAGCAGCAAA  
842 \*  
3001 CATAGatggagaggttgagggctttcgccagaaatgctgtgattctgttattaagtccata  
3061 ccttgtaaataagtgcccttacgtgagtggtcatcaatcagaacctaacacagagtaaa  
3121 ctatgggggaaaaaaaagaagacgaaacagaaactcagggatcactgggagaagccatgg  
3181 cataatcttcaggcaattttagtctgtccaaataaacatacatccttggcatgtaaatca  
3241 tcaagggtaatagtaatatcatatacctgaaacgtgtctcataggagtcctctctgcac

**Figure 2F. The cDNA (SEQ ID NO: 12) and amino acid sequence (SEQ ID NO: 13) of 158P1D7 v.6.**

The start methionine is underlined. The open reading frame extends from nucleic acid 23-1612 including the stop codon.

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1           M K L W I H L F Y S S L L
1  tcggatttcacatgacaacATGAAGCTGTGGATTCATCTCTTTTATTCATCTCTCCT
14  A C I S L H S Q T P V L S S R G S C D S
61  TGCCTGTATATCTTTACTCCAACTCCAGTGCTCTCATCCAGAGGCTCTTGATTC
34  L C N C E E K D G T M L I N C E A K G I
121 TCTTTGCAATTGTGAGGAAAAAGATGGCACAATGCTAATAAATTGTGAAGCAAAAGGTAT
54  K M V S E I S V P P S R P F Q L S L L N
181 CAAGATGGTATCTGAAATAAGTGTGCCACCATCACGACCTTTCCAATAAGCTTATTAA
74  N G L T M L H T N D F S G L T N A I S I
241 TAACGGCTTGACGATGCTTCACACAAATGACTTTTCTGGGCTTACCAATGCTATTTCAT
94  H L G F N N I A D I E I G A F N G L G L
301 ACACCTTGGATTTAACAATATTGCAGATATTGAGATAGGTGCATTAAATGGCCTTGGCCT
114 L K Q L H I N H N S L E I L K E D T F H
361 CCTGAAACAACTTCATATCAATCACAATCTTTAGAAATCTTAAAGAGGATACTTTCCA
134 G L E N L E F L Q A D N N F I T V I E P
421 TGGACTGGAAAACCTGGAATTCCTGCAAGCAGATAACAATTTTATCACAGTGATTGAACC
154 S A F S K L N R L K V L I L N D N A I E
481 AAGTGCCTTTAGCAAGCTCAACAGACTCAAAGTGTTAATTTTAAATGACAATGCTATTGA
174 S L P P N I F R F V P L T H L D L R G N
541 GAGTCTTCTCCAAACATCTTCCGATTGTTCCTTTAACCCATCTAGATCTTCGTGGAAA
194 Q L Q T L P Y V G F L E H I G R I L D L
601 TCAATTACAAACATTGCCTTATGTTGGTTTCTCGAACACATTGGCCGAATATTGGATCT
214 Q L E D N K W A C N C D L L Q L K T W L
661 TCAGTTGGAGGACAACAAATGGGCCTGCAATTGTGACTTATTGCAGTTAAAACTTGGTT
234 E N M P P Q S I I G D V V C N S P P F F
721 GGAGAACATGCCTCCACAGTCTATAATTGGTGATGTTGTCTGCAACAGCCCTCCATTTT
254 K G S I L S R L K K E S I C P T P P V Y
781 TAAAGGAAGTATACTCAGTAGACTAAAGAAGGAATCTATTTGCCCTACTCCACCAGTGTA
274 E E H E D P S G S L H L A A T S S I N D
841 TGAAGAACATGAGGATCCTTCAGGATCATTACATCTGGCAGCAACATCTTCAATAAATGA
294 S R M S T K T T S I L K L P T K A P G L
901 TAGTCGCATGTCAACTAAGACCAGTCCATTCTAAACTACCCACCAAAGCACCAGGTTT
314 I P Y I T K P S T Q L P G P Y C P I P C
961 GATACCTTATATTACAAAGCCATCCACTCAACTCCAGGACCTTACTGCCCTATTCTTG
334 N C K V L S P S G L L I H C Q E R N I E
1021 TAACTGCAAAGTCTATCCCCATCAGGACTTCTAATACATTGTGAGGAGCGCAACATTGA
354 S L S D L R P P P Q N P R K L I L A G N
1081 AAGCTTATCAGATCTGAGACCTCTCCGAAAATCCTAGAAAGCTCATTCTAGCGGGAAA

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374 I I H S L M N P S F G P K H L E E E E E  
1141 TATTATTACAGTTTAAATGAATCCATCCTTTGGTCCAAAGCATCTGGAAGAGGAAGAAGA  
394 R N E K E G S D A K H L Q R S L L E Q E  
1201 GAGGAATGAGAAAGAAGGAAGTGATGCAAAACATCTCCAAAGAAGTCTTTTGGAACAGGA  
414 N H S P L T G S N M K Y K T T N Q S T E  
1261 AAATCATTCACCACTCACAGGGTCAAATATGAAATACAAAACCACGAACCAATCAACAGA  
434 F L S F Q D A S S L Y R N I L E K E R E  
1321 ATTTTATCCTTCCAAGATGCCAGCTCATTGTACAGAAACATTTTAGAAAAAGAAAGGGA  
454 L Q Q L G I T E Y L R K N I A Q L Q P D  
1381 ACTTCAGCAACTGGGAATCACAGAATACCTAAGGAAAAACATTGCTCAGCTCCAGCCTGA  
474 M E A H Y P G A H E E L K L M E T L M Y  
1441 TATGGAGGCACATTATCCTGGAGCCCACGAAGAGCTGAAGTTAATGGAAACATTAATGTA  
494 S R P R K V L V E Q T K N E Y F E L K A  
1501 CTCACGTCCAAGGAAGGTATTAGTGGAACAGACAAAAAATGAGTATTTGAACTTAAAGC  
514 N L H A E P D Y L E V L E Q Q T \*  
1561 TAATTTACATGCTGAACCTGACTATTTAGAAGTCCTGGAGCAGCAAAACATAGatggaga

Figure 3:

Figure 3A. Amino acid sequence 158P1D7 v.1 (SEQ ID NO: 14). The 158P1D7 v.1 protein has 841 amino acids.

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1 MKLWIHLFYS SLLACISLHS QTPVLSSRGs CDSLNCNEEK DGTMLINCEA KGIKMOVSEIS
61 VPPSRPFQLS LLNNGLTMLH TNDFSGLTNA ISIH LGFN NI ADIEIGAFNG LGLLKQLHIN
121 HNSLEILKED TFHGLENL EF LQADNNFITV IEPsAFsKL N RLKVLILNDN AIESLPPNIF
181 RFVPLTHLDL RGNQLQTL PY VGFLEHIGRI LDLQLEDNKW ACNCDLLQLK TWLENMPPQS
241 IIGDVVCNSP PFFKGSILSR LKKESICPTP PVYEEHEDPS GSLHLAATSS INDSRMSTKT
301 TSILKLPTKA PGLIPYITKP STQLPGPYCP IPCNCKVLSP SGLLIHCQER NIESLSDLRP
361 PPQNPRKLIL AGNIIHSLMK SDLVEYFTLE MLHLGNNRIE VLEEGsFMNL TRLQKLYLNG
421 NHLTKLSKGM FLGLHNLEYL YLEYNAIKEI LPGTFNPM PK LKVLYLNNNL LQVLPPHIFS
481 GVPLTKVNLK TNQFTHLPVS NILDDL DLT QIDLEDNPWD CSCDLVGLQQ WIQKLSKNTV
541 TDDILCTSPG HLDKKELKAL NSEILCPGLV NNPSMPTQTS YLMVTT PATT TNTADTILRS
601 LTDAVPLSVL ILGLLIMFIT IVFCAAGIVV LVLHRRRRYK KKQVDEQMRD NSPVHLQYSM
661 YGHKTTHHTT ERPSASLYEQ HMVSPMVH VY RSPSFGPKHL EEEEEERNEKE GSDAKHLQRS
721 LLEQENHSPL TGSNMKYKTT NQSTEFSLFQ DASSLYRNIL EKERELQQLG ITEYLRKNIA
781 QLQPDMEAHY PGAHEELKLM ETLMSRPRK VLVEQTKNEY FELKANLHAE PDYLEVLEQQ
841 T

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Figure 3B. Amino acid sequence 158P1D7 v.3 (SEQ ID NO: 15). The 158P1D7 v.3 protein has 732 amino acids.

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1 MKLWIHLFYS SLLACISLHS QTPVLSSRGs CDSLNCNEEK DGTMLINCEA KGIKMOVSEIS
61 VPPSRPFQLS LLNNGLTMLH TNDFSGLTNA ISIH LGFN NI ADIEIGAFNG LGLLKQLHIN
121 HNSLEILKED TFHGLENL EF LQADNNFITV IEPsAFsKL N RLKVLILNDN AIESLPPNIF
181 RFVPLTHLDL RGNQLQTL PY VGFLEHIGRI LDLQLEDNKW ACNCDLLQLK TWLENMPPQS
241 IIGDVVCNSP PFFKGSILSR LKKESICPTP PVYEEHEDPS GSLHLAATSS INDSRMSTKT
301 TSILKLPTKA PGLIPYITKP STQLPGPYCP IPCNCKVLSP SGLLIHCQER NIESLSDLRP
361 PPQNPRKLIL AGNIIHSLMK SDLVEYFTLE MLHLGNNRIE VLEEGsFMNL TRLQKLYLNG
421 NHLTKLSKGM FLGLHNLEYL YLEYNAIKEI LPGTFNPM PK LKVLYLNNNL LQVLPPHIFS
481 GVPLTKVNLK TNQFTHLPVS NILDDL DLT QIDLEDNPWD CSCDLVGLQQ WIQKLSKNTV
541 TDDILCTSPG HLDKKELKAL NSEILCPGLV NNPSMPTQTS YLMVTT PATT TNTADTILRS
601 LTDAVPLSVL ILGLLIMFIT IVFCAAGIVV LVLHRRRRYK KKQVDEQMRD NSPVHLQYSM
661 YGHKTTHHTT ERPSASLYEQ HMGAEELKL METLMSRPR KVLVEQTKNE YFELKANLHA
721 EPDYLEVLEQ QT

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Figure 3C. Amino acid sequence 158P1D7 v.4 (SEQ ID NO: 16). The 158P1D7 v.4 protein has 395 amino acids.

```

1 MKLWIHLFYS SLLACISLHS QTPVLSSRGs CDSLNCNEEK DGTMLINCEA KGIKMOVSEIS
61 VPPSRPFQLS LLNNGLTMLH TNDFSGLTNA ISIH LGFN NI ADIEIGAFNG LGLLKQLHIN
121 HNSLEILKED TFHGLENL EF LQADNNFITV IEPsAFsKL N RLKVLILNDN AIESLPPNIF
181 RFVPLTHLDL RGNQLQTL PY VGFLEHIGRI LDLQLEDNKW ACNCDLLQLK TWLENMPPQS
241 IIGDVVCNSP PFFKGSILSR LKKESICPTP PVYEEHEDPS GSLHLAATSS INDSRMSTKT

```

301 TSILKLPTKA PGLIPYITKP STQLPGPYCP IPCNCKVLSP SGLLIHCQER NIESLSDLRP  
361 PPQNPRKLIL AGNIIHSLMK SILWSKASGR

**Figure 3D. Amino acid sequence 158P1D7 v.6 (SEQ ID NO: 17).** The 158P1D7 v.6 protein has 529 amino acids.

1 MKLWIHLFYS SLLACISLHS QTPVLSSRGS CDSLNCNEEK DGTMLINCEA KGIKMVSEIS  
61 VPPSRPFQLS LLNNGLTMLH TNDFSGLTNA ISIH LGFN NI ADIEIGAFNG LGLLKQLHIN  
121 HNSLEILKED TFHGLENLEF LQADNNFITV IEP SAFSKLN RLKVLILNDN AIESLPPNIF  
181 RFVPLTHLDL RGNQLQTL PY VGFLEHIGRI LDLQLEDNKW ACNCDLLQLK TWLENMPPQS  
241 IIGDVVCNSP PFFKGSILSR LKKESICPTP PVYEEHEDPS GSLHLAATSS INDSRMSTKT  
301 TSILKLPTKA PGLIPYITKP STQLPGPYCP IPCNCKVLSP SGLLIHCQER NIESLSDLRP  
361 PPQNPRKLIL AGNIIHSLMN PSFGPKHLEE EEERNEKEGS DAKHLQRSLL EQENHSPLTG  
421 SNMKYKTTNQ STEFLSFQDA SSLYRNILEK ERELQQLGIT EYLRKNIAQL QPDMEAHYPG  
481 AHEELKLMET LMYSRPRKVL VEQTKNEYFE LKANLHAEPD YLEVLEQQT



**Figure 4: 158P1D7 v.1 amino acid (SEQ ID NO: 18) BLAST homology to hypothetical protein FLJ22774 (SEQ ID NO: 19).**

Identities = 798/798 (100%)

```

Query: 44  MLINCEAKGIKMVSEISVPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI 103
           MLINCEAKGIKMVSEISVPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI
Sbjct: 1    MLINCEAKGIKMVSEISVPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI 60

Query: 104 EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRK 163
           EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRK
Sbjct: 61  EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRK 120

Query: 164  VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPYVGFLEHIGRILDQLEDNKWACN 223
           VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPYVGFLEHIGRILDQLEDNKWACN
Sbjct: 121 VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPYVGFLEHIGRILDQLEDNKWACN 180

Query: 224  CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRKKESICPTPPVYEEHEDPSGSL 283
           CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRKKESICPTPPVYEEHEDPSGSL
Sbjct: 181 CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRKKESICPTPPVYEEHEDPSGSL 240

Query: 284  HLAATSSINDSRMSTKTTSSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 343
           HLAATSSINDSRMSTKTTSSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL
Sbjct: 241 HLAATSSINDSRMSTKTTSSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 300

Query: 344  LIHCQERNIESLSDLRPPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNNRIVELE 403
           LIHCQERNIESLSDLRPPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNNRIVELE
Sbjct: 301 LIHCQERNIESLSDLRPPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNNRIVELE 360

Query: 404  EGSFMNTRLQKLYLNGNHLTKLSKGMFLGLHNLEYLYLEYNAIKEILPGTFNPMPLKV 463
           EGSFMNTRLQKLYLNGNHLTKLSKGMFLGLHNLEYLYLEYNAIKEILPGTFNPMPLKV
Sbjct: 361 EGSFMNTRLQKLYLNGNHLTKLSKGMFLGLHNLEYLYLEYNAIKEILPGTFNPMPLKV 420

Query: 464  LYLNNLLQVLPPHIFSGVPLTKVNLKTNQFTHLPVSNILDDLDTQIDLEDNPWDCSC 523
           LYLNNLLQVLPPHIFSGVPLTKVNLKTNQFTHLPVSNILDDLDTQIDLEDNPWDCSC
Sbjct: 421 LYLNNLLQVLPPHIFSGVPLTKVNLKTNQFTHLPVSNILDDLDTQIDLEDNPWDCSC 480

Query: 524  DLVGLQQWIQKLSKNTVTDDILCTSPGHLDKKELKALNSEILCPGLVNNPSMPTQTSYLM 583
           DLVGLQQWIQKLSKNTVTDDILCTSPGHLDKKELKALNSEILCPGLVNNPSMPTQTSYLM
Sbjct: 481 DLVGLQQWIQKLSKNTVTDDILCTSPGHLDKKELKALNSEILCPGLVNNPSMPTQTSYLM 540

Query: 584  VTTPATTTNTADTILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLVHRRRRYKKKQ 643
           VTTPATTTNTADTILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLVHRRRRYKKKQ
Sbjct: 541 VTTPATTTNTADTILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLVHRRRRYKKKQ 600

Query: 644  VDEQMRDNSPVHLQYSMYGHKTTHHTTERPSASLYEQHMVSPMVHVYRSPSFGPKHLEEE 703
           VDEQMRDNSPVHLQYSMYGHKTTHHTTERPSASLYEQHMVSPMVHVYRSPSFGPKHLEEE
Sbjct: 601 VDEQMRDNSPVHLQYSMYGHKTTHHTTERPSASLYEQHMVSPMVHVYRSPSFGPKHLEEE 660

Query: 704  EERNEKEGSDAKHLQRSLLQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYRNILEKE 763
           EERNEKEGSDAKHLQRSLLQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYRNILEKE
Sbjct: 661 EERNEKEGSDAKHLQRSLLQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYRNILEKE 720

Query: 764  RELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTKNEYFEL 823
           RELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTKNEYFEL
Sbjct: 721 RELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTKNEYFEL 780

Query: 824  KANLHAEPDYLEVLEQQT 841
           KANLHAEPDYLEVLEQQT
Sbjct: 781 KANLHAEPDYLEVLEQQT 798

```

Figure 5:

Figure 5A: Alignment of 158P1D7 v.1 (SEQ ID NO: 20) with human FLJ22774, CLONE KAIA1575.[Homo sapiens] (SEQ ID NO: 21)

Identities = 405/415 (97%), Positives = 405/415 (97%)

```

158P1D7: 44 MLINCEAKGIKMVSEISVPPSRPFQLSLLNGLTMLHTNDFSGLTNAISIHFGFNFIADI 103
              MLINCEAKGIKMVSEISVPPSRPFQLSLLNGLTMLHTNDFSGLTNAISIHFGFNFIADI
Sbjct: 1      MLINCEAKGIKMVSEISVPPSRPFQLSLLNGLTMLHTNDFSGLTNAISIHFGFNFIADI 60

158P1D7:104 EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENEFLQADNNFITVIEPSAFSKLNRLK 163
              EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENEFLQADNNFITVIEPSAFSKLNRLK
Sbjct: 61     EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENEFLQADNNFITVIEPSAFSKLNRLK 120

158P1D7:164 VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPHYVGFLHIGRILDQLQEDNKWACN 223
              VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPHYVGFLHIGRILDQLQEDNKWACN
Sbjct: 121    VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPHYVGFLHIGRILDQLQEDNKWACN 180

158P1D7:224 CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRLKKESICPTPPVYEEHEDPSGSL 283
              CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRLKKESICPTPPVYEEHEDPSGSL
Sbjct: 181    CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRLKKESICPTPPVYEEHEDPSGSL 240

158P1D7:284 HLAATSSINDSRMSTKTTSSILKLPKAPGLIPYITKPTQLPGPYCPIPCNCKVLSPSGL 343
              HLAATSSINDSRMSTKTTSSILKLPKAPGLIPYITKPTQLPGPYCPIPCNCKVLSPSGL
Sbjct: 241    HLAATSSINDSRMSTKTTSSILKLPKAPGLIPYITKPTQLPGPYCPIPCNCKVLSPSGL 300

158P1D7:344 LIHCQERNIESLSDLRPPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNNRIEVLE 403
              LIHCQERNIESLSDLRPPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNNRIEVLE
Sbjct: 301    LIHCQERNIESLSDLRPPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNNRIEVLE 360

158P1D7:404 EGSFMNLTRELQKLYLNGNHLTKLSKGMFLGLHXXXXXXXXXXAIKEILPGTFNPM 458
              EGSFMNLTRELQKLYLNGNHLTKLSKGMFLGLH          AIKEILPGTFNPM
Sbjct: 361    EGSFMNLTRELQKLYLNGNHLTKLSKGMFLGLHNLLEYLYLEYNAIKEILPGTFNPM 415

```

Figure 5b: Alignment of 158P1D7 v.1 protein (SEQ ID NO: 22) with a human protein similar to IGFALS (SEQ ID NO: 23)

Identities = 316/864 (36%), Positives = 459/864 (52%)

```

158P1D7:1    MKLWIHLFYSSLLACISLHSQTPVLSSRGSCDSLNCCEKDGTMLINCEAKGIKMVSEIS 60
              M LW+ L S+L++ + S V          ++C+C + + +NCE + +++
Sbjct: 17    MFLWLFLILSALISSTNADSDISV-----EICNVCSVCVSVENVLYVNCVKSVYRPNQLK 71

158P1D7:61   VPPSRPFQLSLLNGLTMLHTNDFSGLTNAISIHFGFNFIADI EIGAFNGLGLLKQLHIN 120
              P S + L+ NN L +L+ N F ++A+S+HLG N + +IE GAF GL LKQLH+N
Sbjct: 72    PPWSNFYHLNFQNNFLNLYPNTFLNFHAVSLHLGNNKLQNI EGGAFLGLSALKQLHLN 131

158P1D7:121  HNSLEILKEDTFHGLENEFLQADNNFITVIEPSAFSKLNRLKVLILNDNAIESLPPNIF 180
              +N L+IL+ DTF G+ENLE+LQAD N I IE AF+KL++LKVLILNDN I LP NIF
Sbjct: 132   NNELKILRADTFGLGIENLEYLQADYNLIK YIERGAFNKLHKLKVLILNDNLISFLPDNIF 191

158P1D7:181  RFVPLTHLDLRGNQLQTLPHYVGFLHIGRILDQLQEDNKWACNCDLLQLKTWLENMPPQS 240
              RF LTHLD+RGN++Q LPY+G LEHIGR+++LQLEDN W C+CDLL LK WLENMP
Sbjct: 192   RFASLTHLDIRGNRIQKLPYIGVLEHIGRVVELQLEDNPWNCSCDLLPLKAWLENMPYNI 251

158P1D7:241  IIGDVVCNSPPFFKGSILSRLKKESICP-----TPPVYEEHEDPSGSLHLAATS 289
              IG+ +C +P G +L K+ +CP          PP E+ + + H TS
Sbjct: 252   YIGEAICETPSDLYGRLLKETNKQELCPMGTSDFDVRILPPSQLENGYTTPNGHTTQTS 311

158P1D7:290  SINDSRMSTKTTSSILKLPKAPGLI-----PYITKPTQLPG-PYCPIPCNCKV- 337
              KTT+ P+K G++ I T++P CP PC CK
Sbjct: 312   LHRLVTKPPKTTN----PSKISGIVAGKALSNNRNLQIVSYQTRVPLTPCPAPCFCKTH 367

158P1D7:338  LSPSGLLIHCQERNIESLSDLRPPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNN 397
              S GL ++CQE+NI+S+S+L P P N +KL + GN I + SD ++ L++LHLG+N
Sbjct: 368   PSDLGLSVNCQEKNIQSMSELIPKPLNAKHLHVNGNSIKDQVDVSDFTDFEGLDLLHLGNS 427

158P1D7:398  RIEVLEEGSFMNLTRELQKLYLNGNHLTKLSKGMFLGLHXXXXXXXXXXAIKEILPGTFNP 457
              +I V++ F NLT L++LYLNGN + +L +F GLH          IKEI GTF+
Sbjct: 428   QITVIKGDVFHNLTLNRRLYLNGNQIERLYPEIFSGLHNLQYLYLEYNLIKEISAGTFDS 487

```

158P1D7:458 MXXXXXXXXXXXXXXXXXHFSGVPLTKVNLKTNQFTHLPVSNIXXXXXXXXXXXXXXN 517  
M +IFSG PL ++NL+ N+F +LPVS + N  
Sbjct: 488 MPNLQLLYLNNNLLKSLPVYIFSGAPLARLNLNRNNKFMYLPVSGVLDQLQSLTQIDLEG 547

158P1D7:518 PWDCSCDLVGLQQWIQKLSKNTVTDDILCTSPGHLDDKKELKALNSEILCPGLVNNPSMPT 577  
PWDC+CDLV L+ W++KLS V ++ C +P ELK+L +EILCP L+N PS P  
Sbjct: 548 PWDCTCDLVALKLWVEKLSDGIVVKELKCETPVQFANIELKSLKNEILCPKLLNKPSAP- 606

158P1D7:578 QTSYLMVXXXXXXXXXXXXXILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLVLRHRR 637  
+ I VPLS+LIL +L++ I VF A ++V VL R +  
Sbjct: 607 ---FTSPAPAITFTTPLGPIRSPPGGPVPLSILILSILVVLILTTFVAFCLLVFLRRNK 663

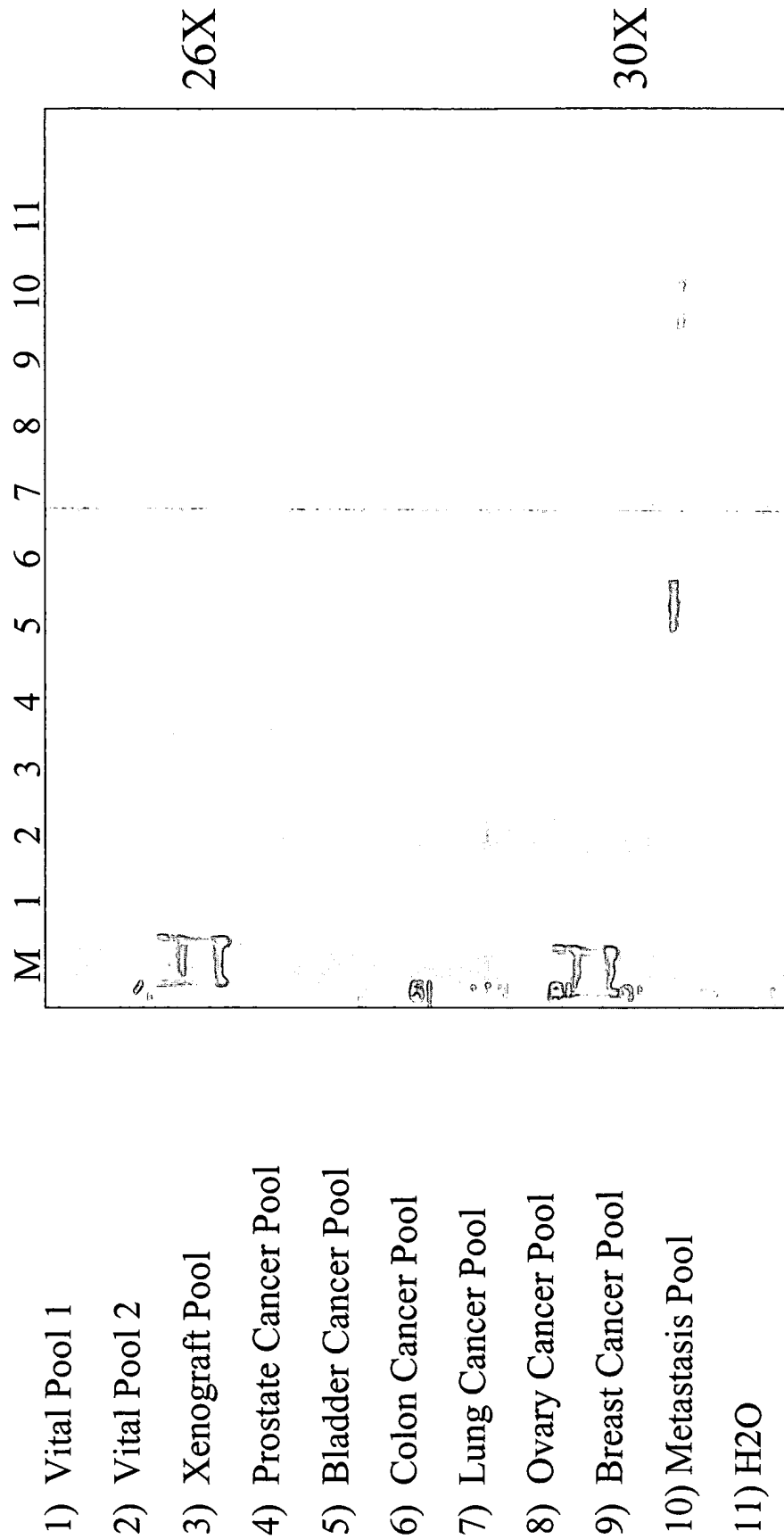
158P1D7:638 RYKKKQVDEQMRDNSPVHLQYSMYGHKTTHHTTERPSASLYEQHMVSPMVHVYRSPSFGP 697  
+ K D + LQ + HK T + E + + +S + G  
Sbjct: 664 KPVTVKHEGLGNPDGSMQLQLRKHDHK-----TNKKDGLSTEAFIPQTIEQMSKSHTCGL 718

158P1D7:698 KHLXXXXXXXXXXGSDAKHLQRSLLSEQENHSPLTGSNMKYKTTNQSTEFSLFQDASSLYR 757  
K G K + R++ ++E + + T ++ E +D++ +  
Sbjct: 719 KESETGFMFSDPPGQ--KVMRNVADKEKDLLHVDTRKRLSTIDELDELFP SRDSNVFIQ 776

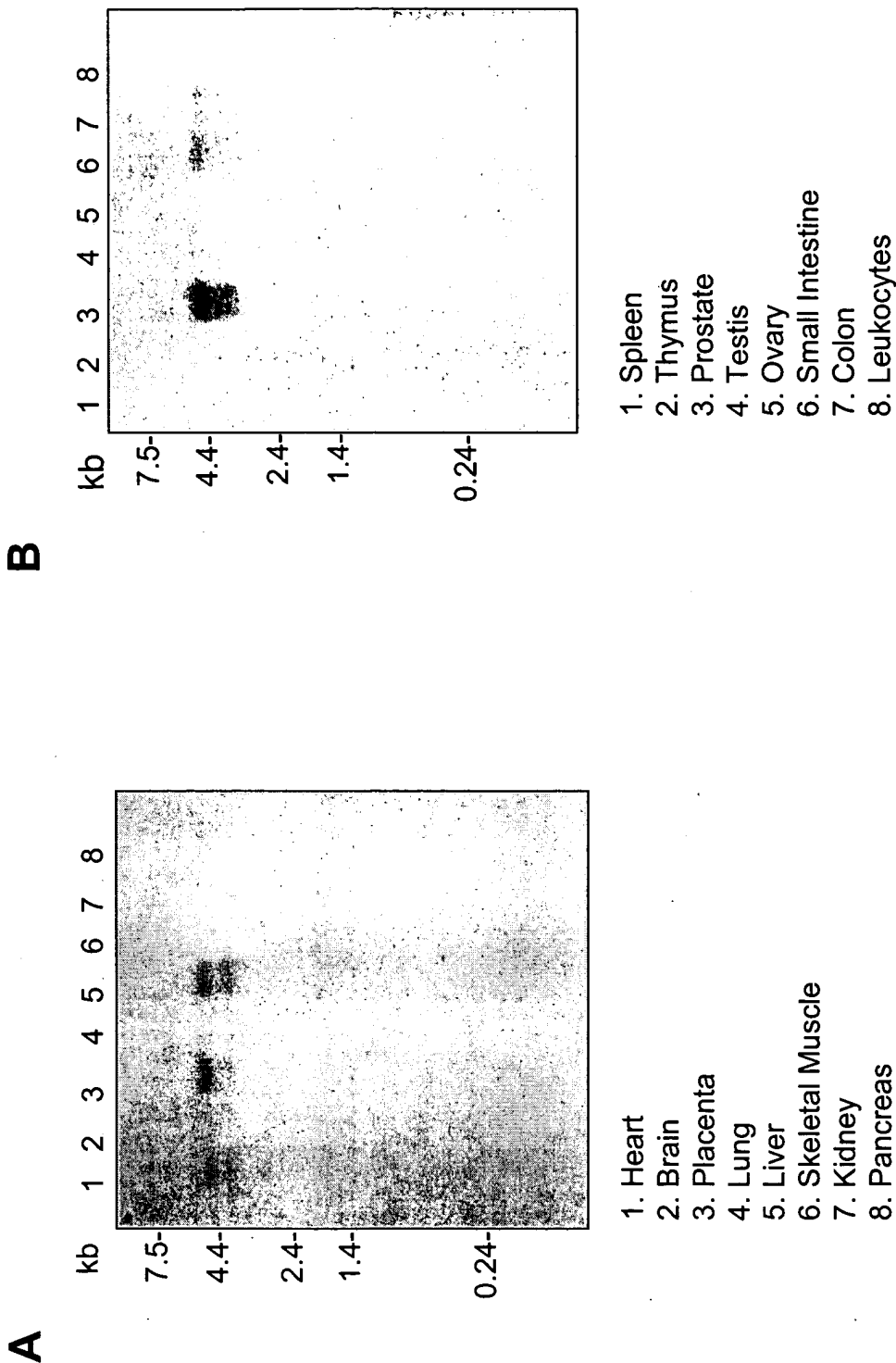
158P1D7:758 NILEKERELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTK 817  
N LE ++E +G++ + E YP + K ++L+ K++VEQ K  
Sbjct: 777 NFLESKKEYNSIGVSGF-----EIRYPEKQPDKSKKSLIGNHNSKIVVEQRK 824

158P1D7:818 NEYFELKANLHAEPDYLEVLEQQT 841  
+EYFELKA L + PDYL+VLE+QT  
Sbjct: 825 SEYFELKAKLQSSPDYLQVLEEQT 848

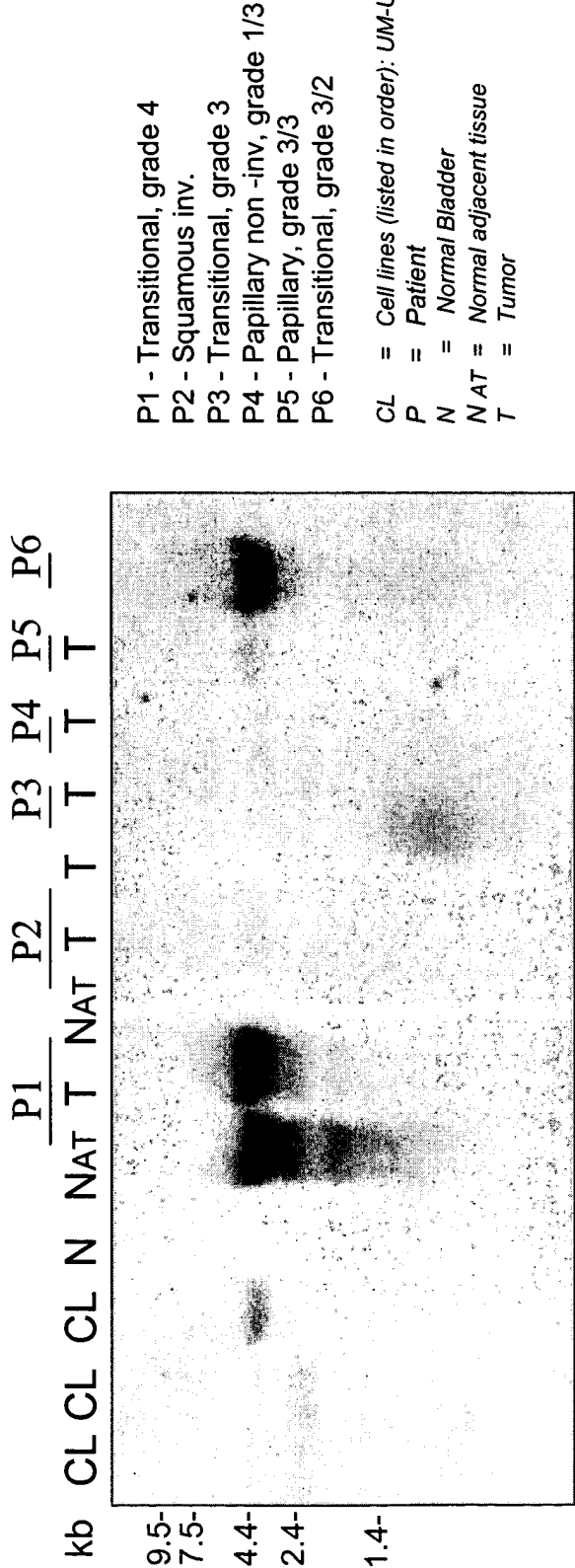
**Figure 6. Expression of 158P1D7 by RT-PCR**



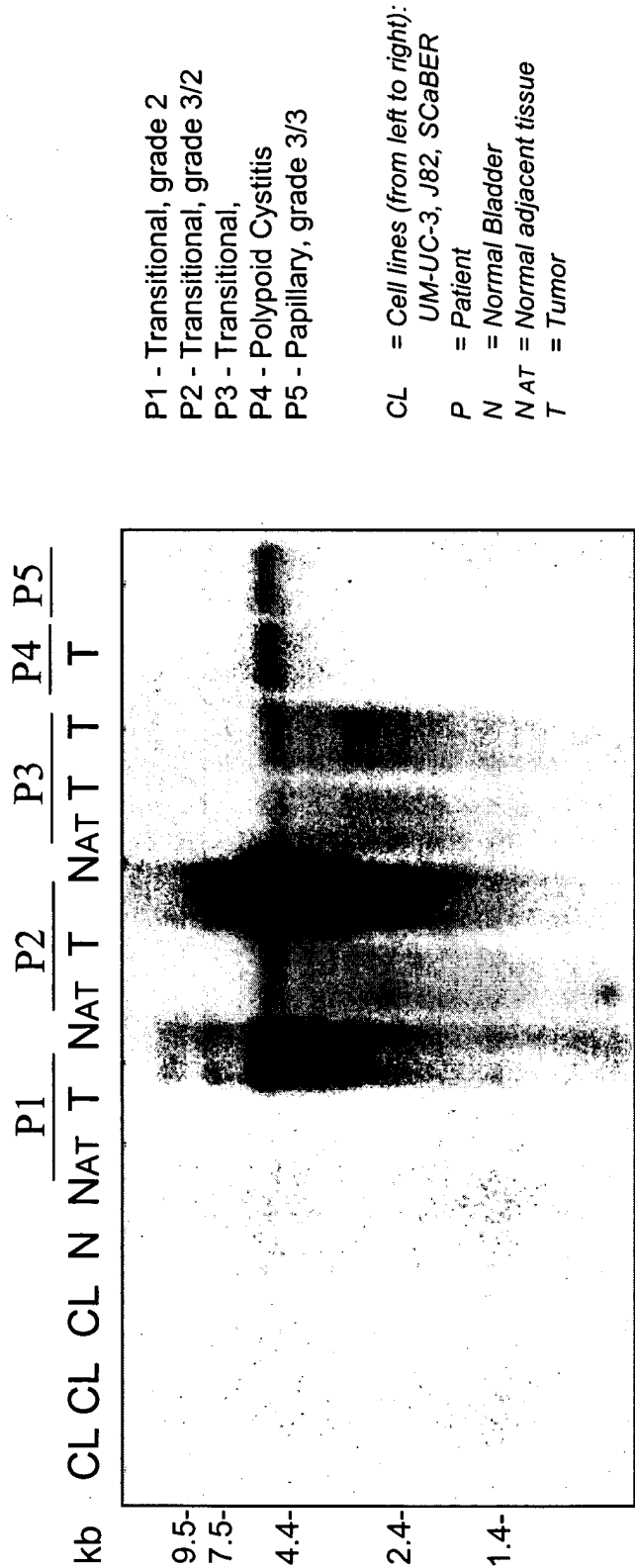
**Figure 7. Expression of 158P1D7 in Normal Tissues**



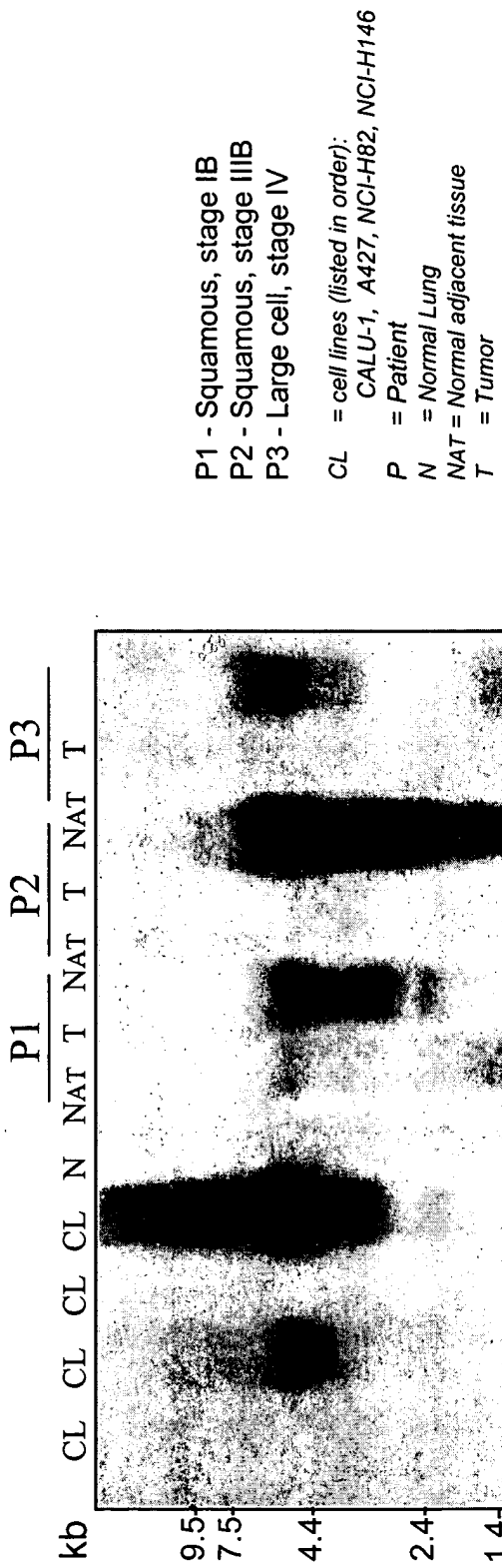
**Figure 8A.** Expression of 158P1D7 in Bladder Cancer Patient Specimens



**Figure 8B.** Expression of 158P1D7 in Bladder Cancer Patient Specimens

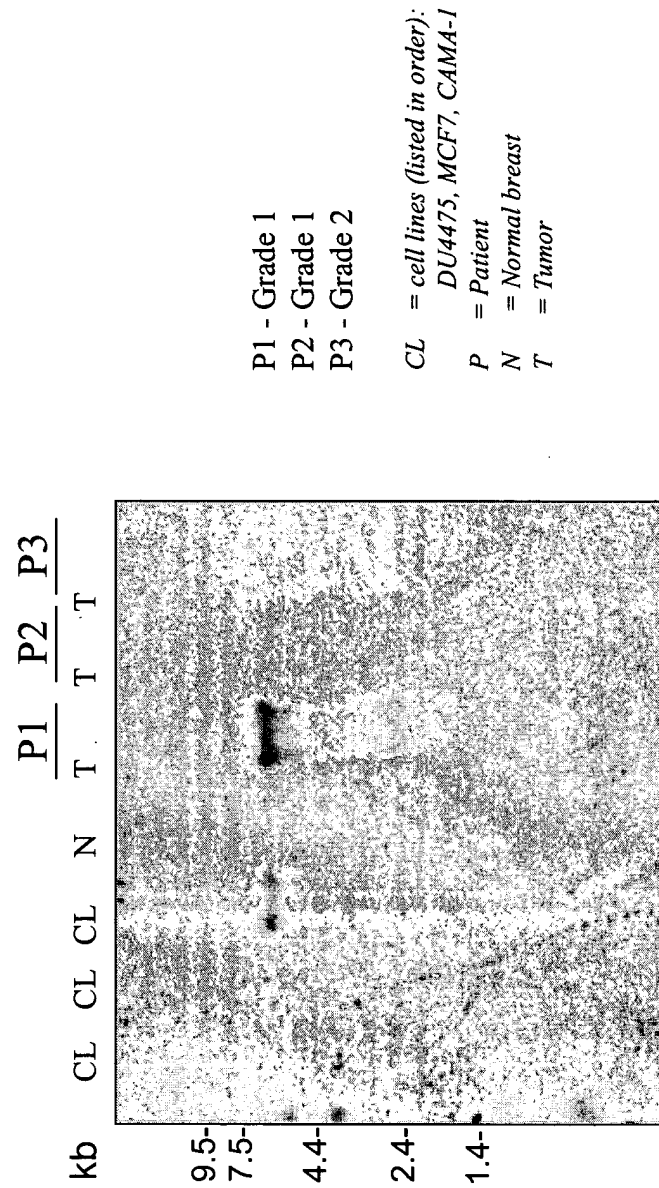


## **Figure 9.**





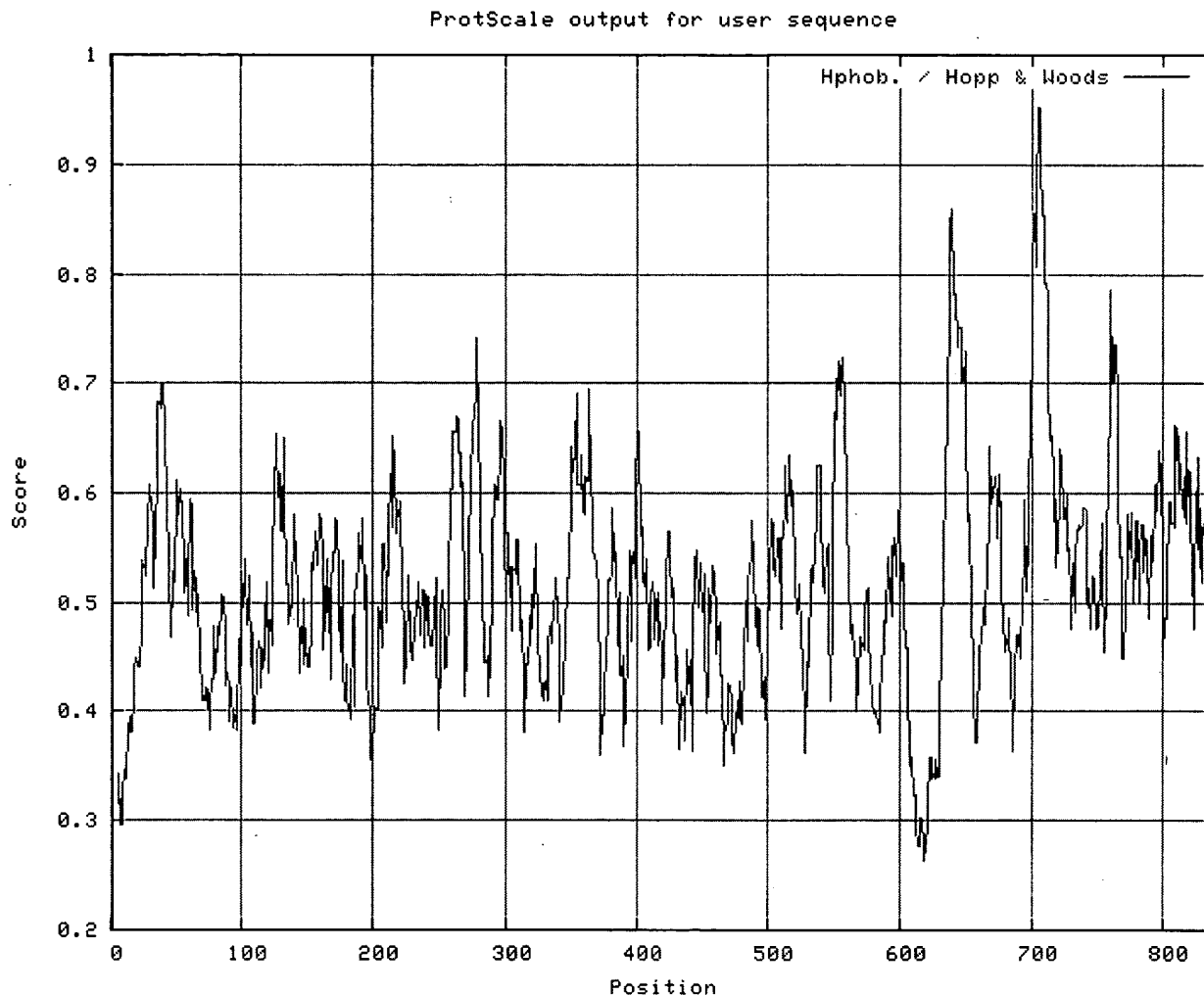
**Figure 10. Expression of 158P1D7 in Breast Cancer Patient Specimens**



# Figure 11a - 158P1D7 variant 1

## Hydrophilicity profile

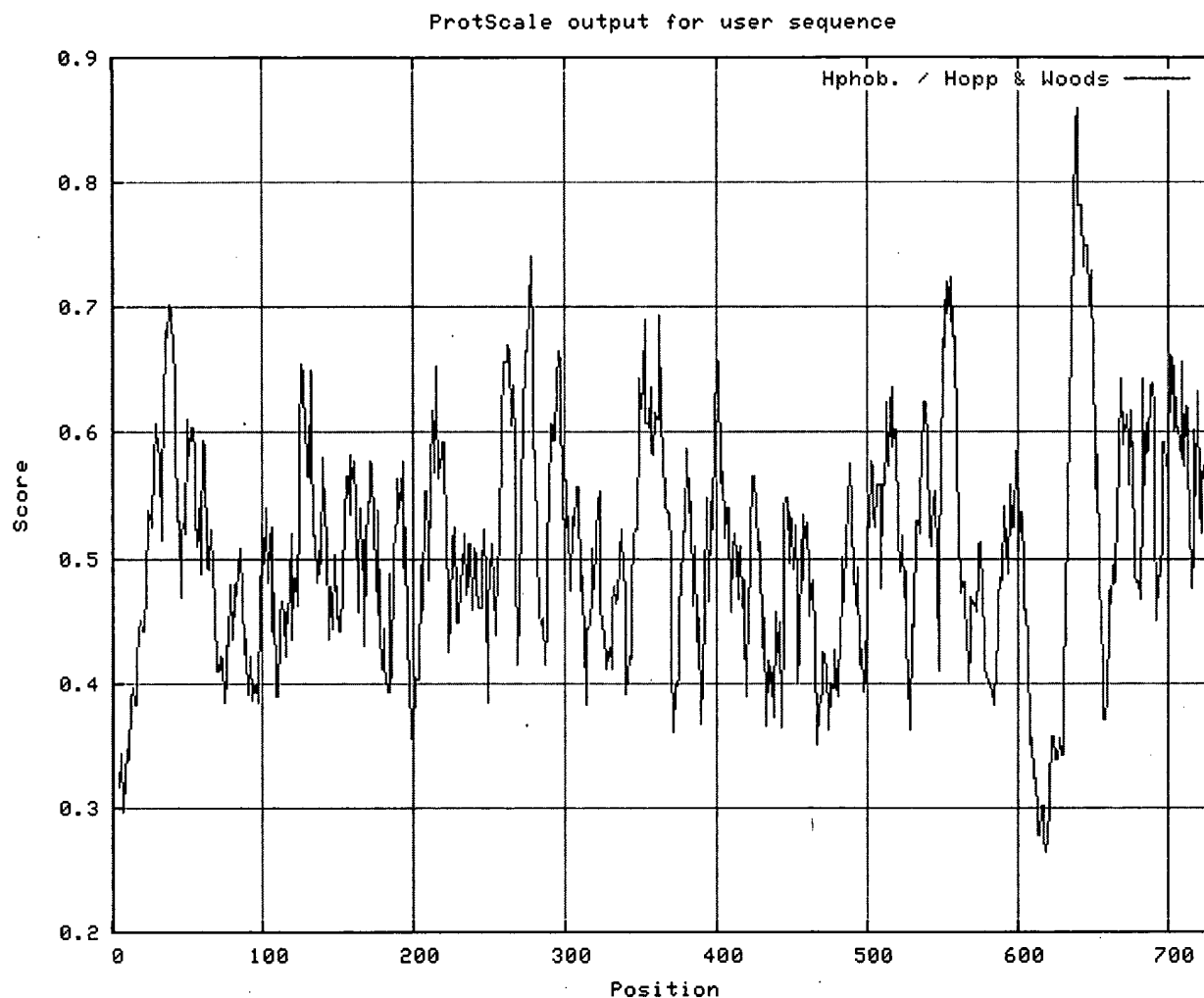
(Hopp T.P., Woods K.R., 1981.  
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)



# Figure 11b - 158P1D7 variant 3

## Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981.  
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

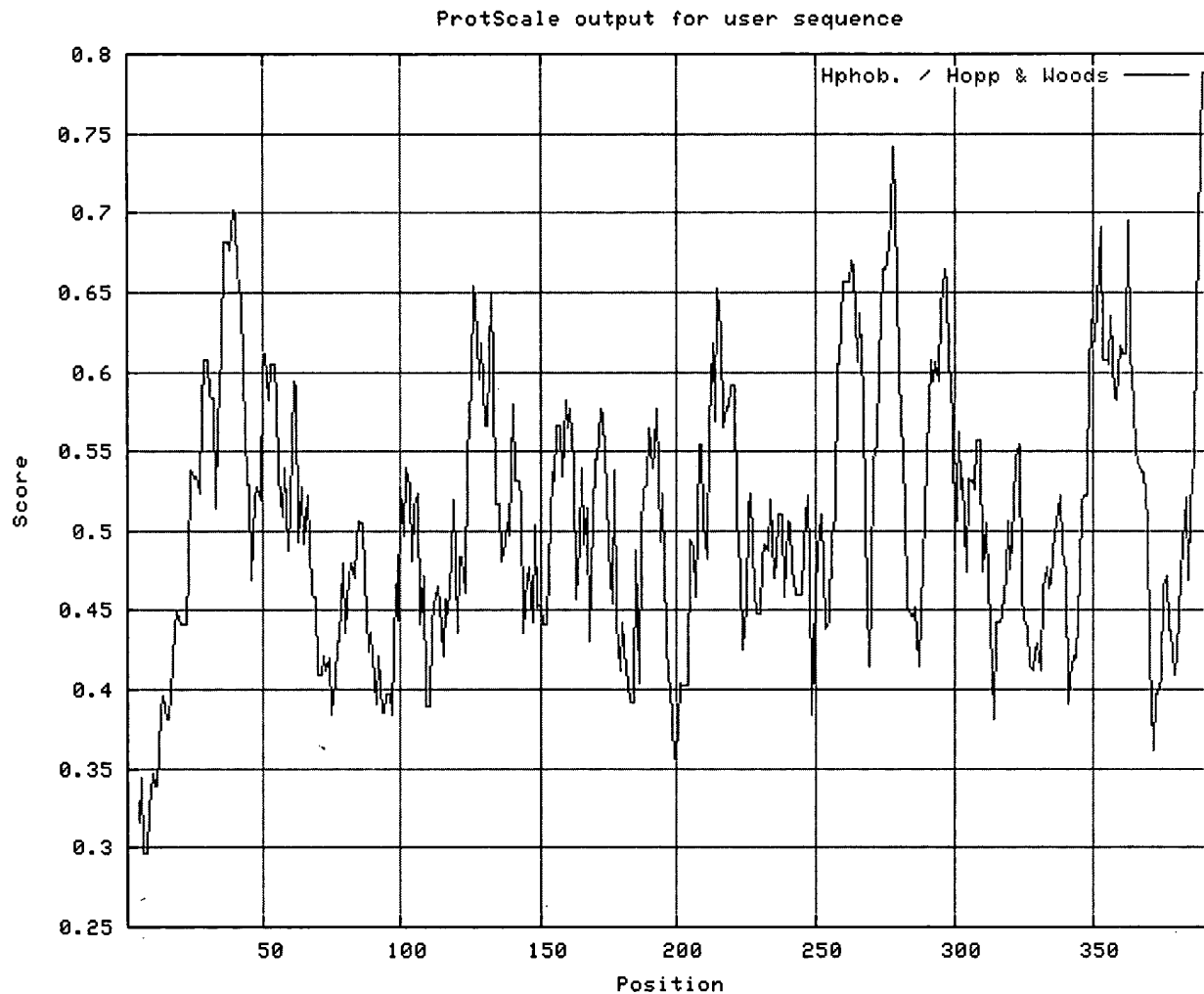


# Figure 11c - 158P1D7 variant 4

## Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981.

Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

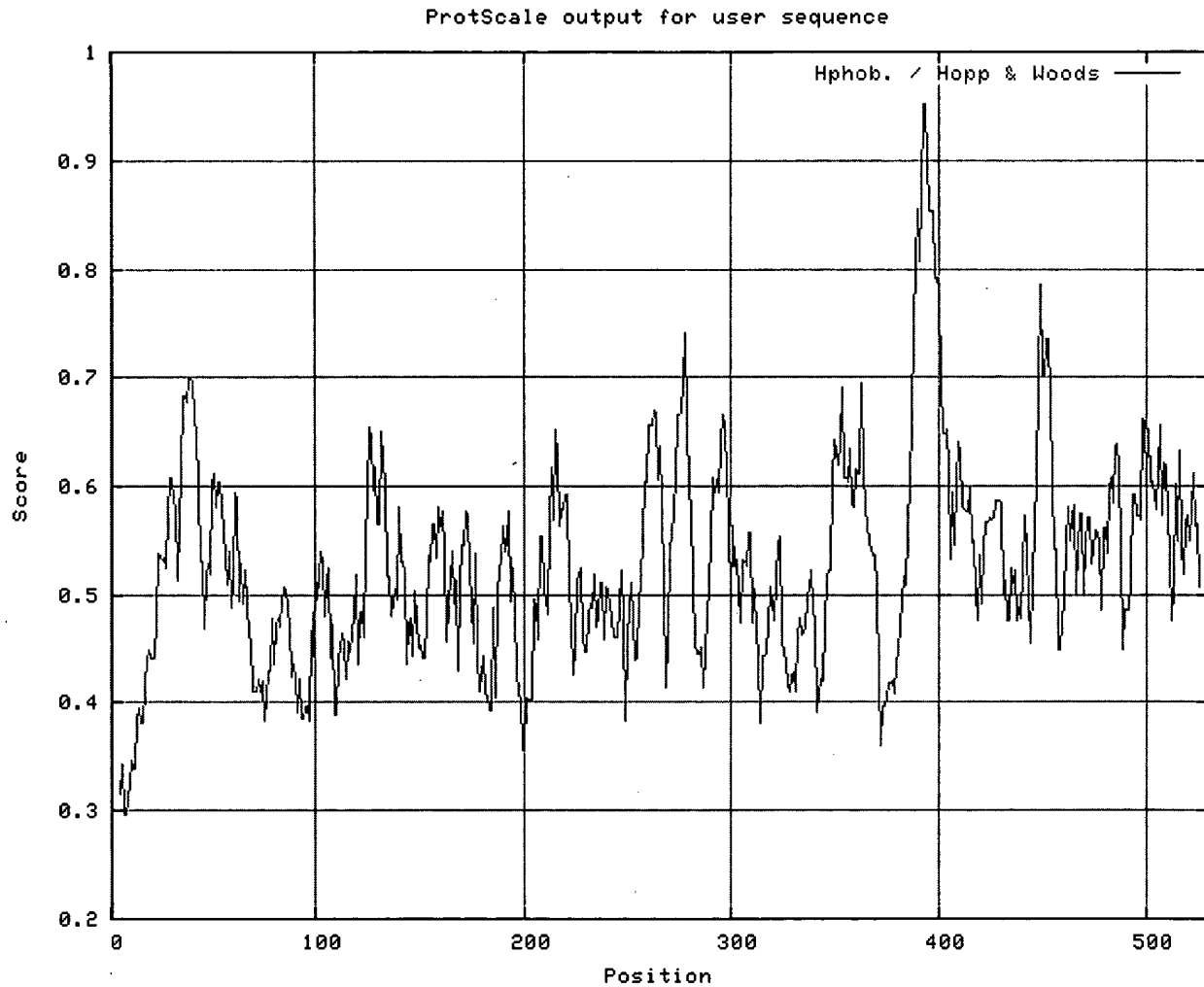


## Figure 11d - 158P1D7 variant 6

### Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981.

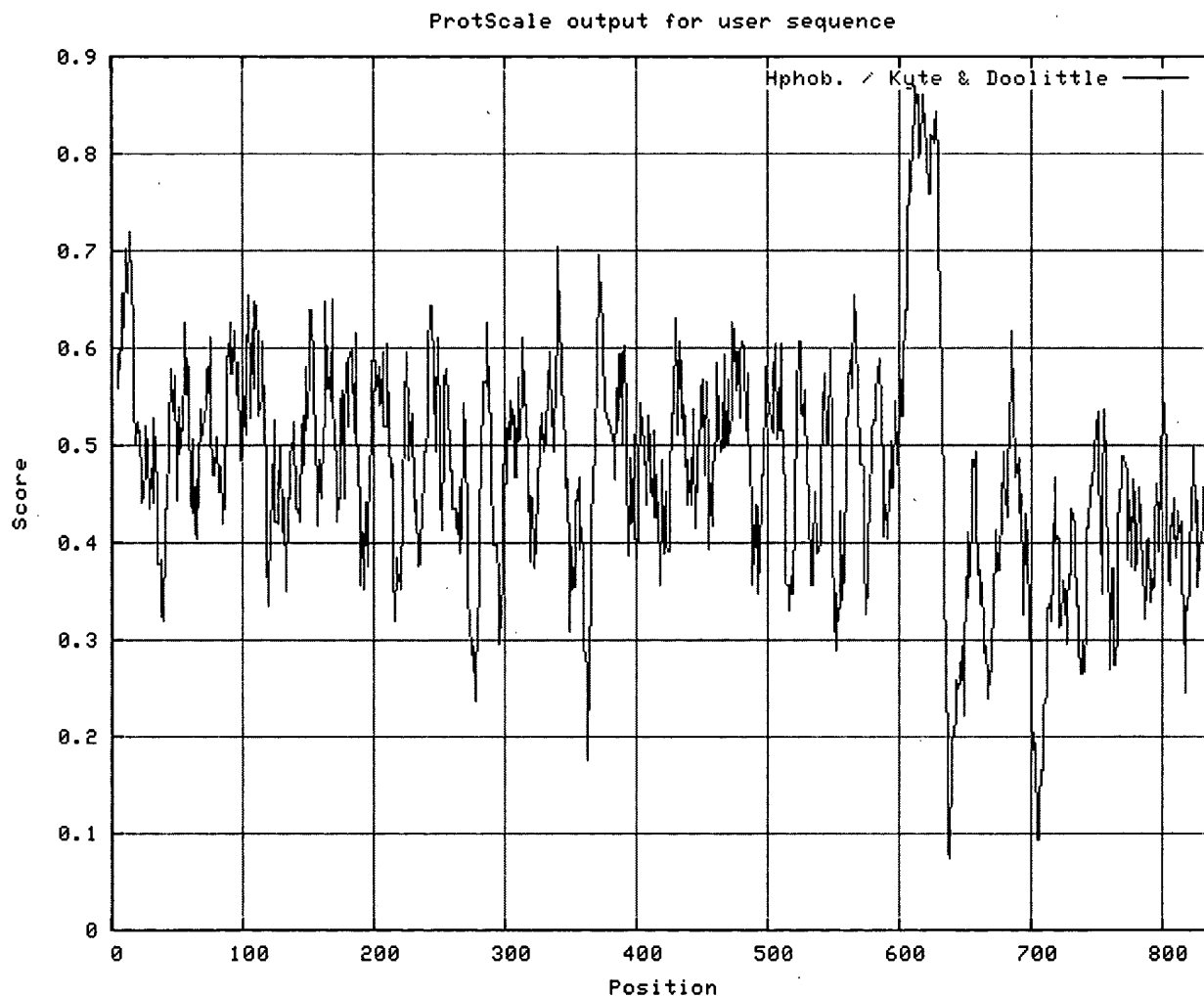
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)



# Figure 12a - 158P1D7 variant 1

## Hydropathicity Profile

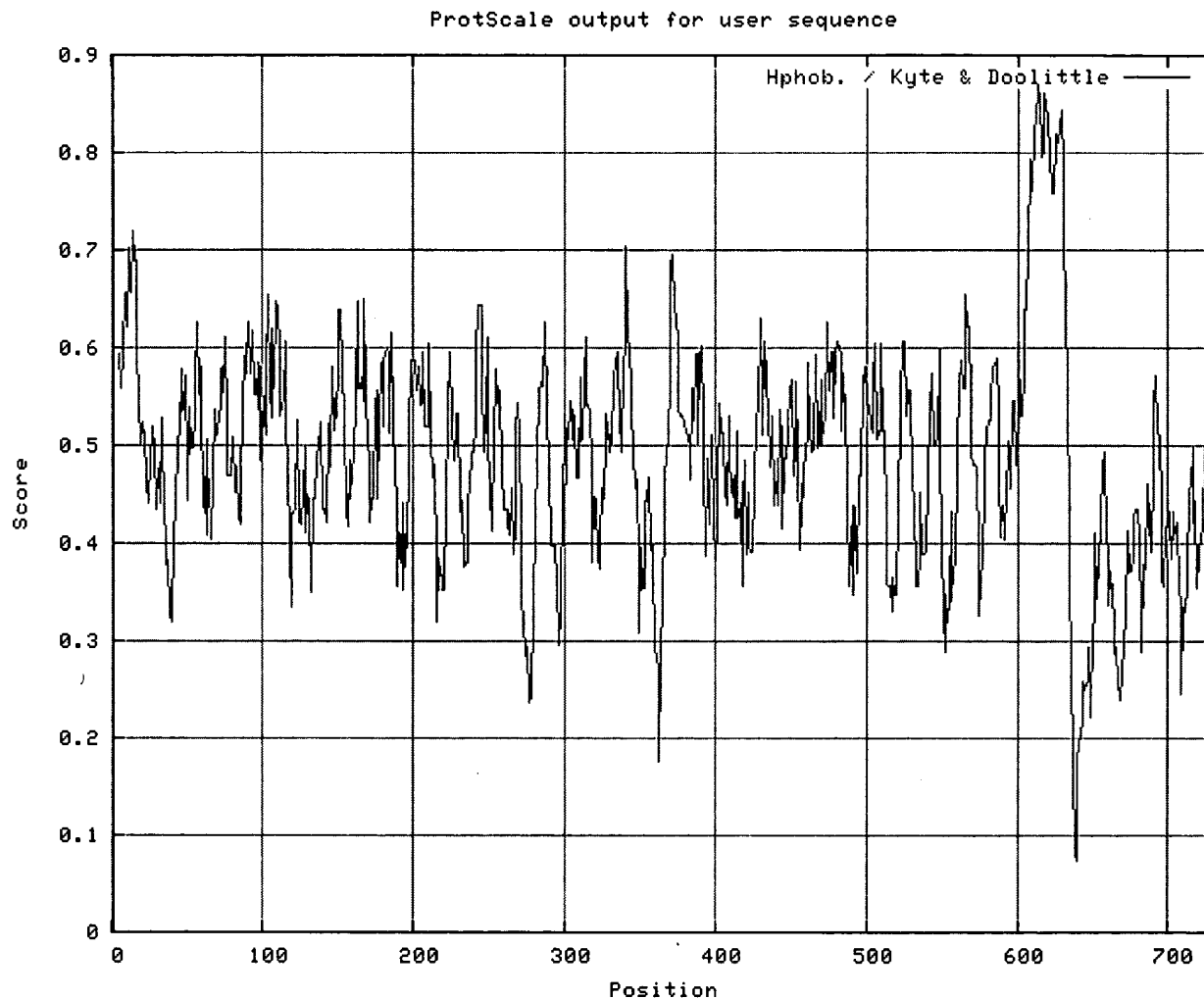
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)



# Figure 12b - 158P1D7 variant 3

## Hydropathicity Profile

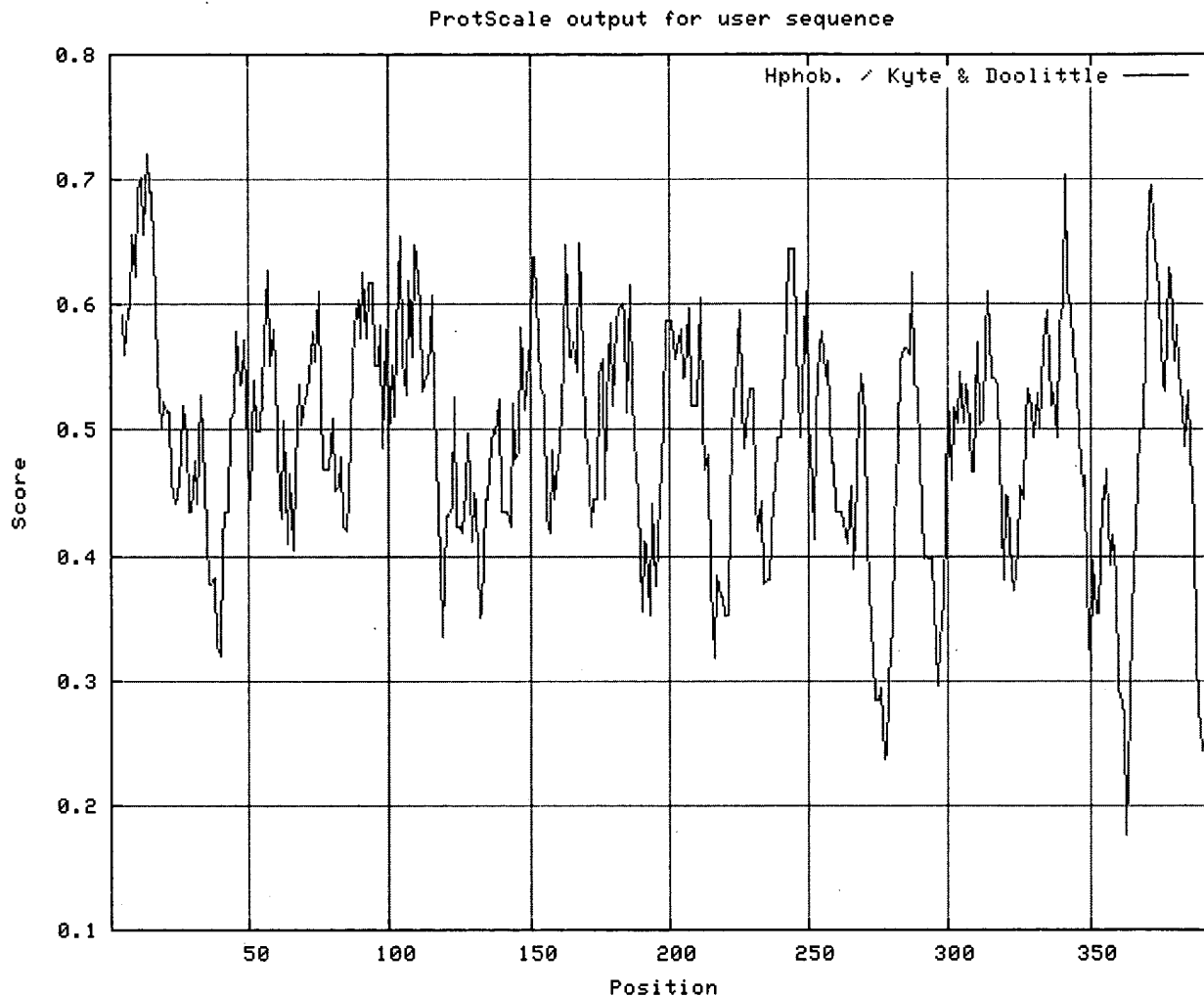
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)



# Figure 12c - 158P1D7 variant 4

## Hydropathicity Profile

(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

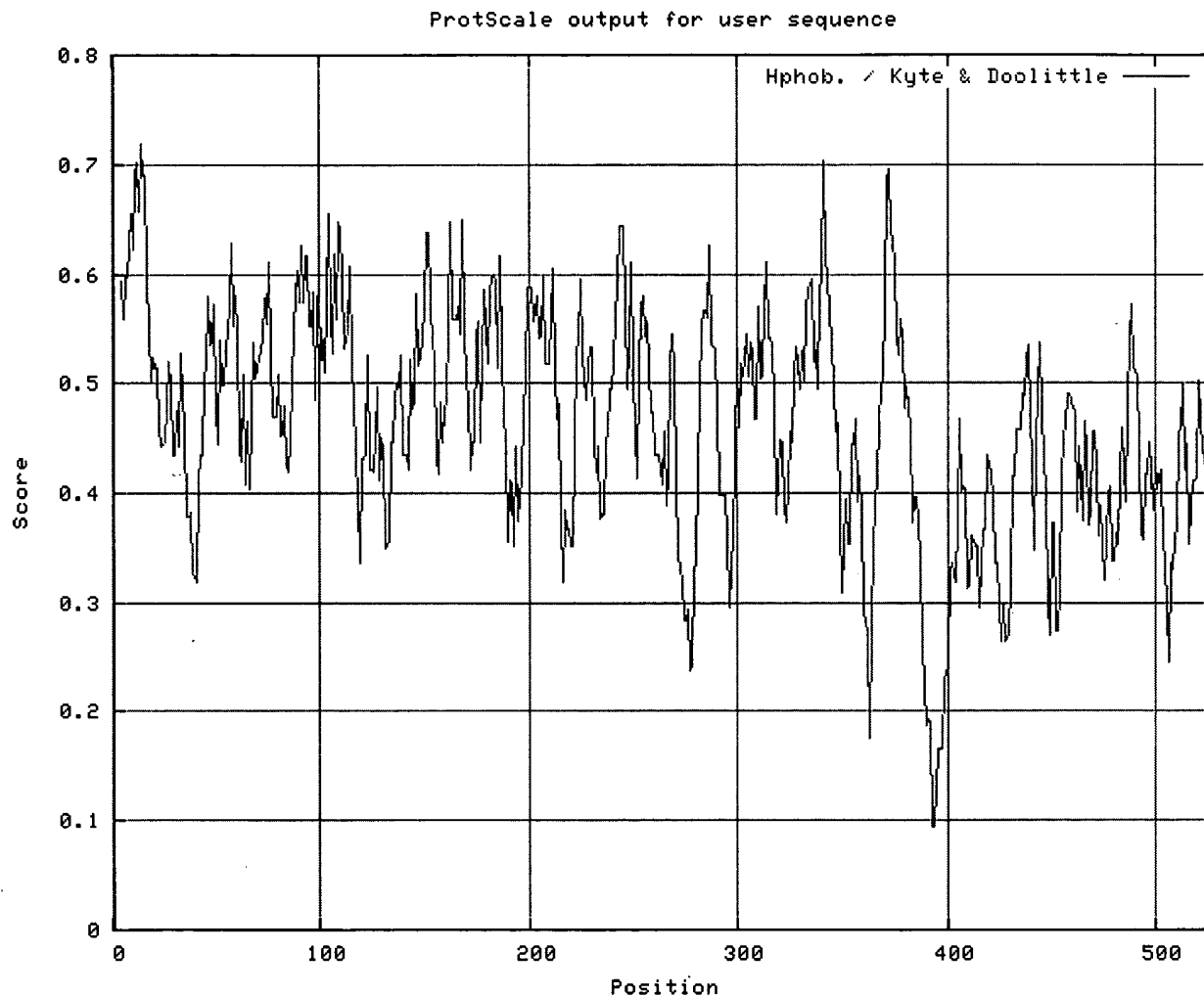




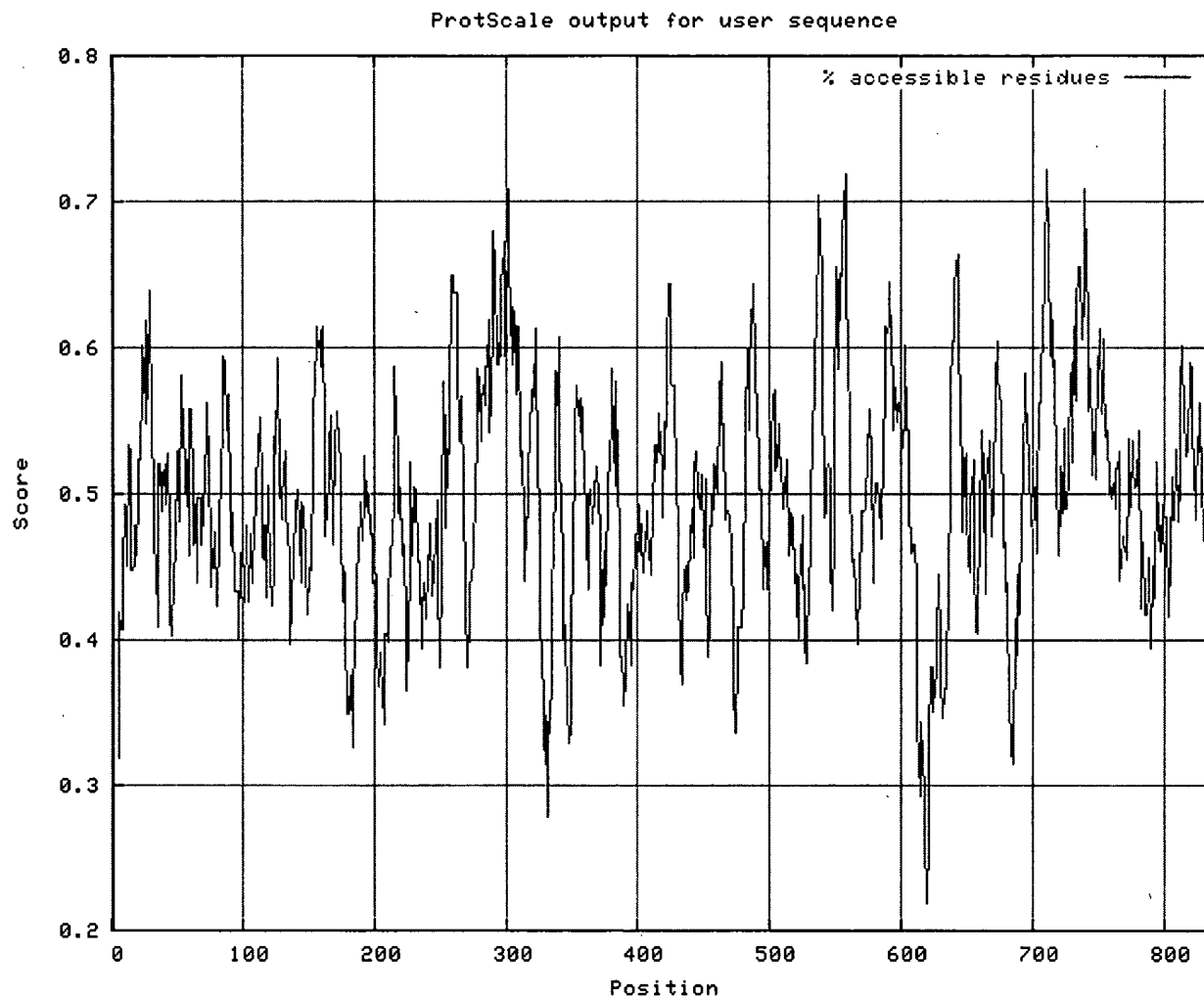
# Figure 12d - 158P1D7 variant 6

## Hydropathicity Profile

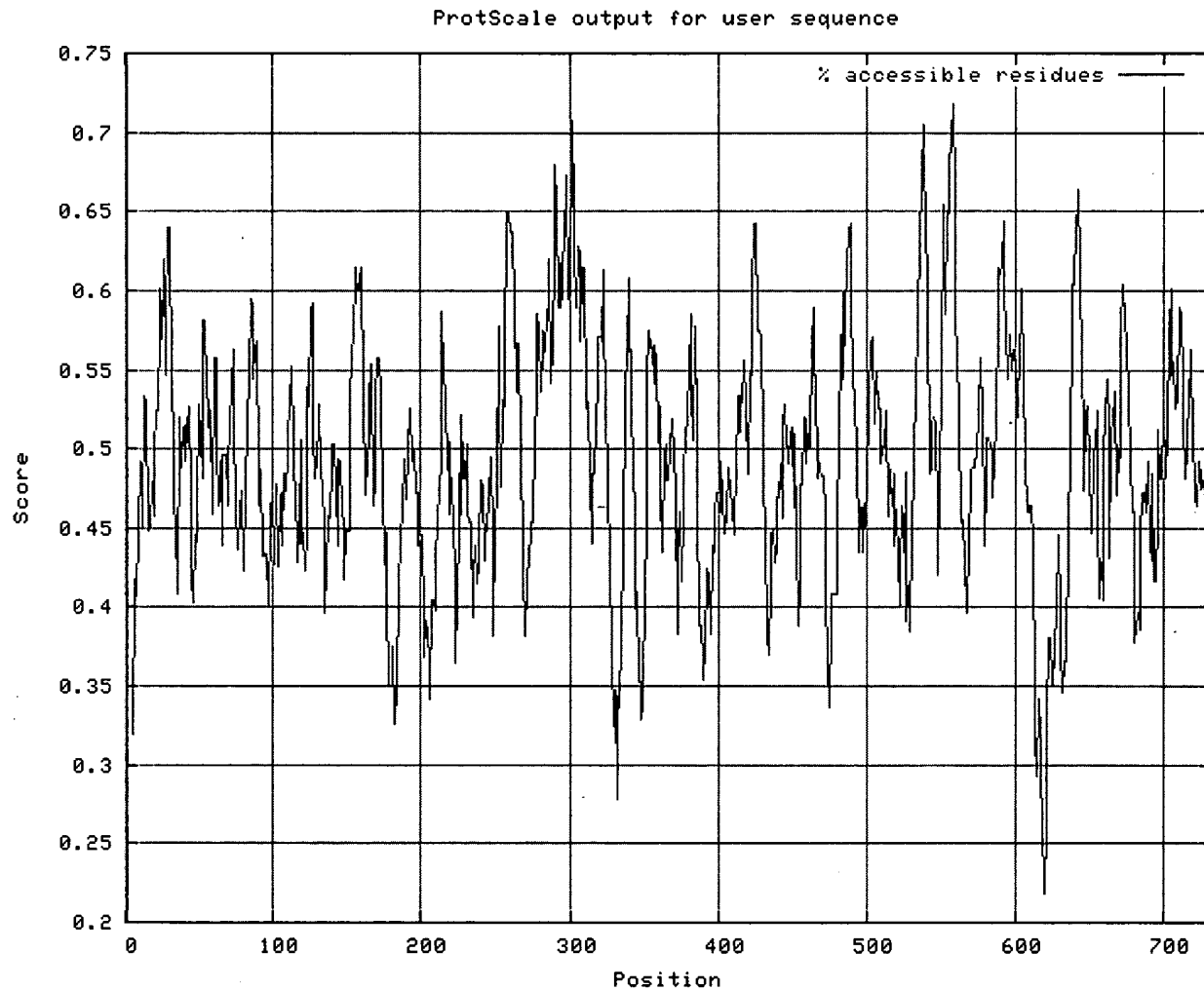
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)



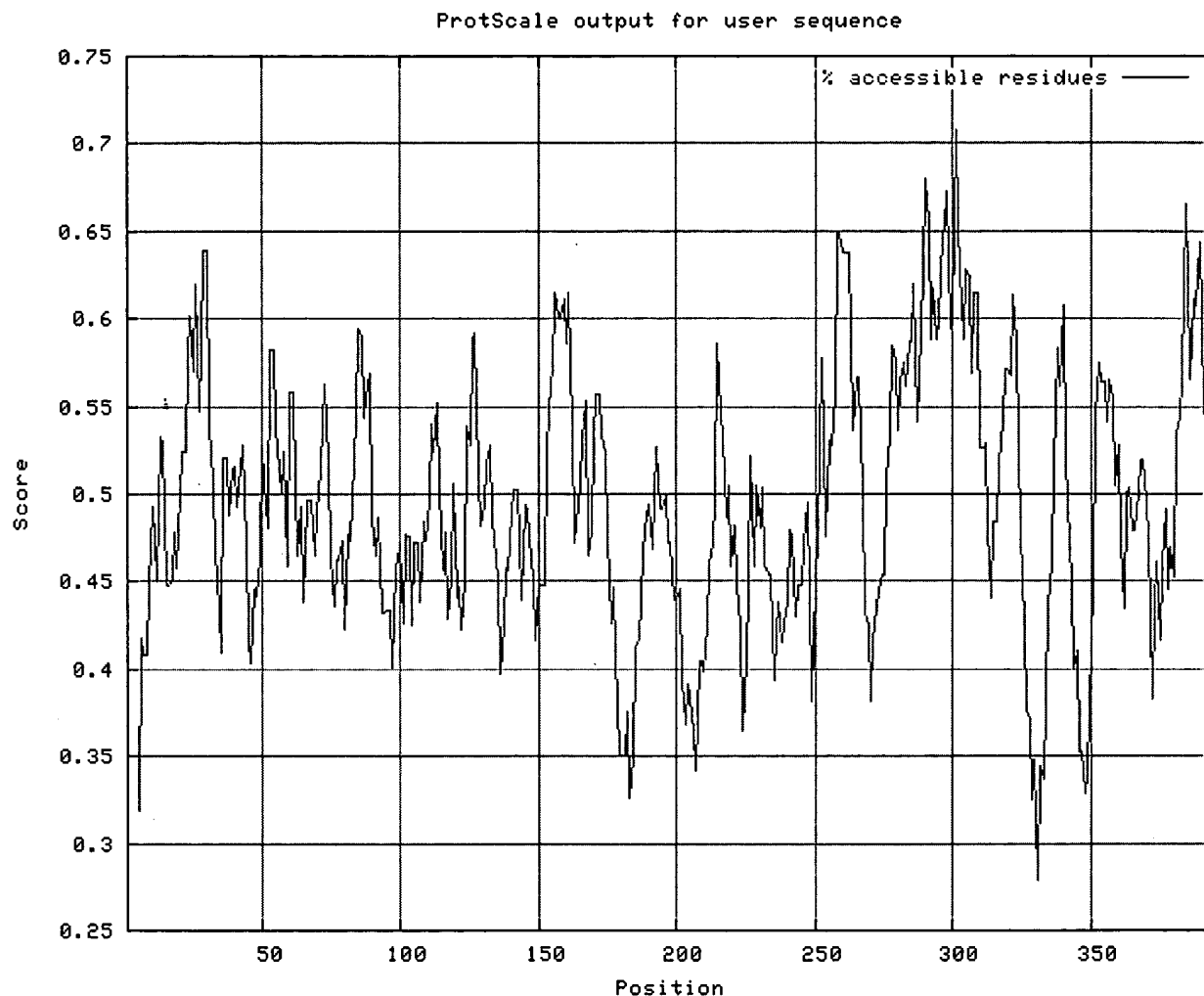
# Figure 13a - 158P1D7 variant 1 % Accessible Residues Profile (Janin J., 1979. Nature 277:491-492)



# Figure 13b - 158P1D7 variant 3 % Accessible Residues Profile (Janin J., 1979. Nature 277:491-492)



# Figure 13c - 158P1D7 variant 4 % Accessible Residues Profile (Janin J., 1979. Nature 277:491-492)



# Figure 13d - 158P1D7 variant 6 % Accessible Residues Profile (Janin J., 1979. Nature 277:491-492)

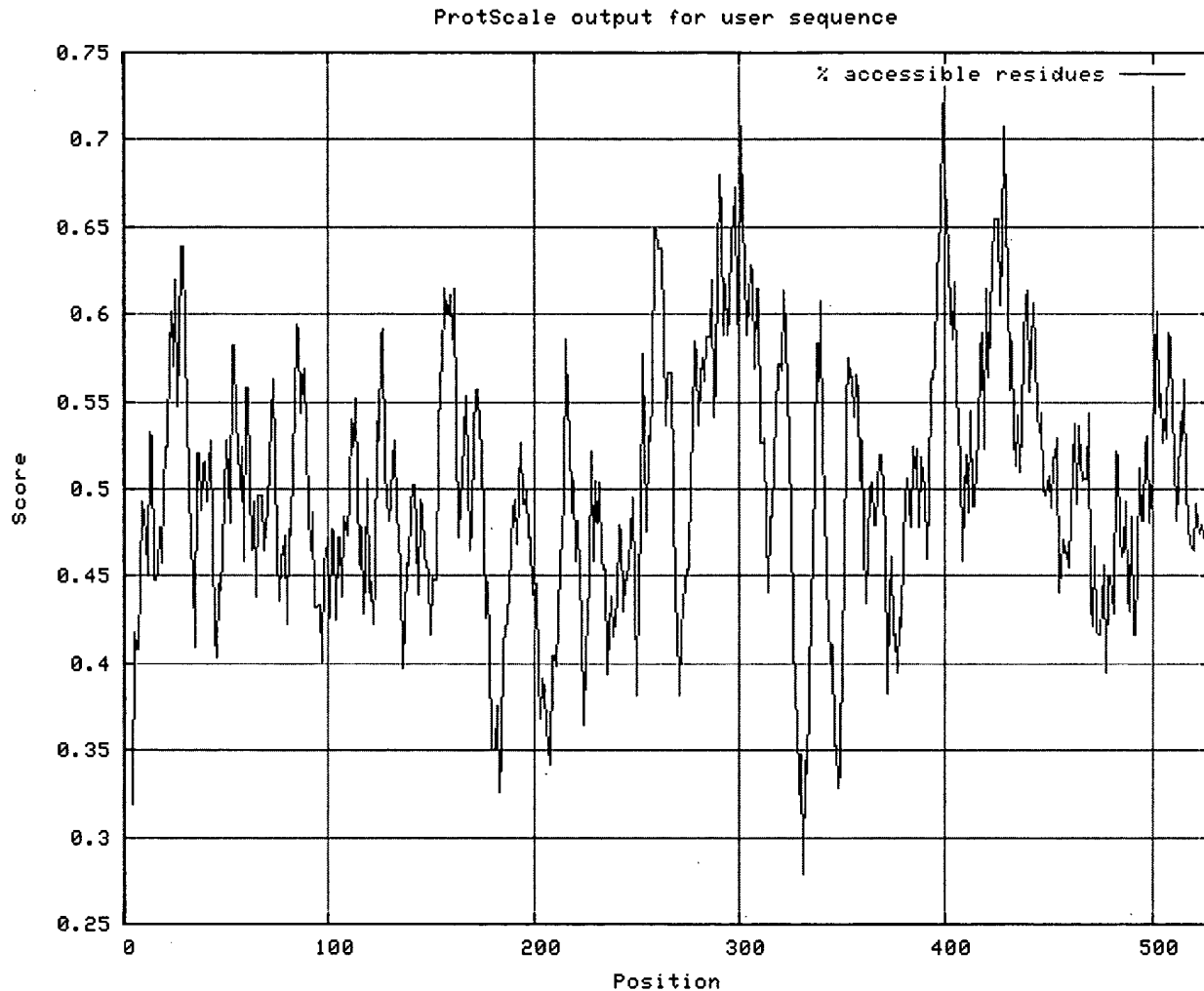


Figure 14a - 158P1D7 variant 1  
Average Flexibility Profile  
(Bhaskaran R., Ponnuswamy P.K., 1988.  
Int. J. Pept. Protein Res. 32:242-255)

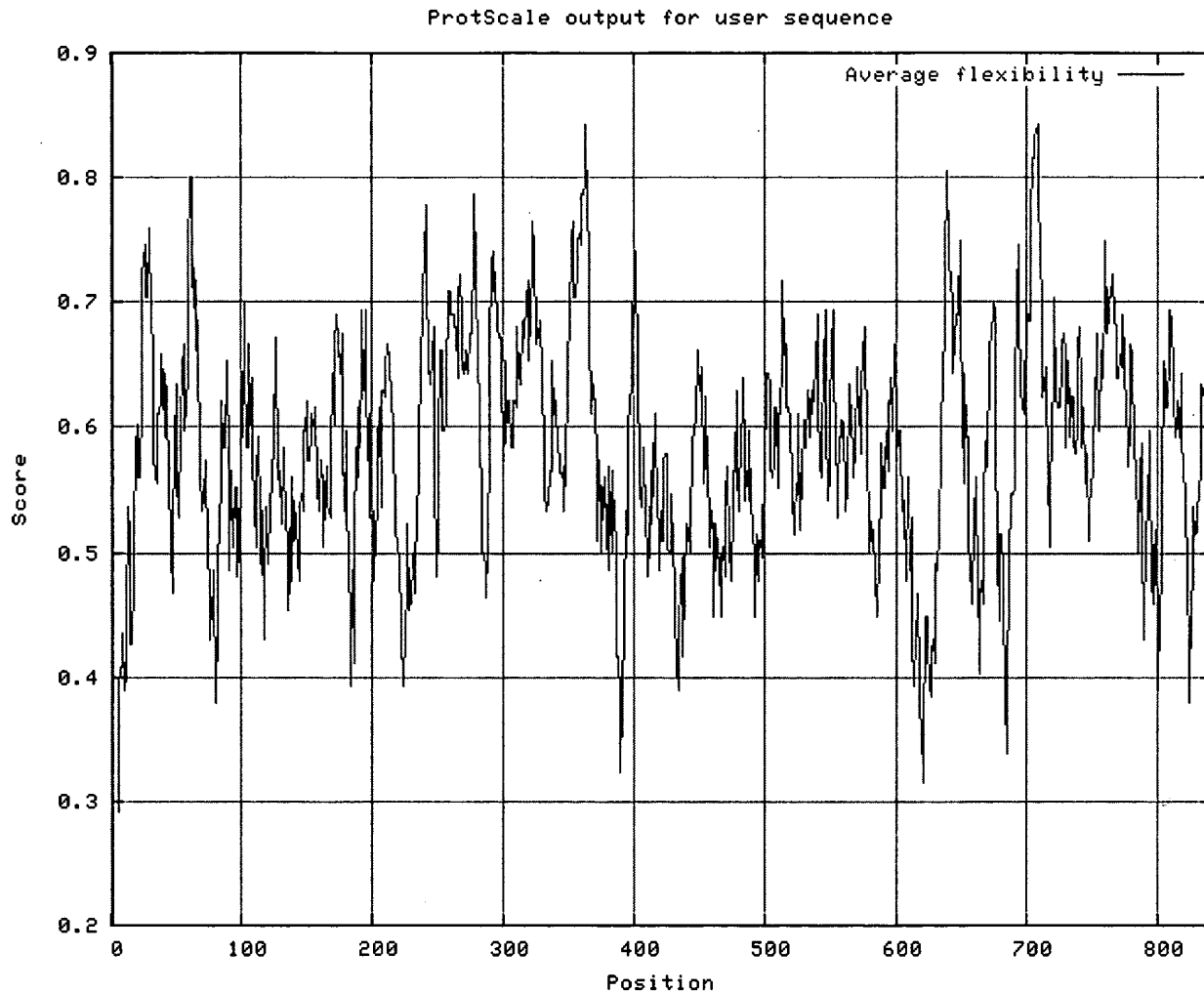
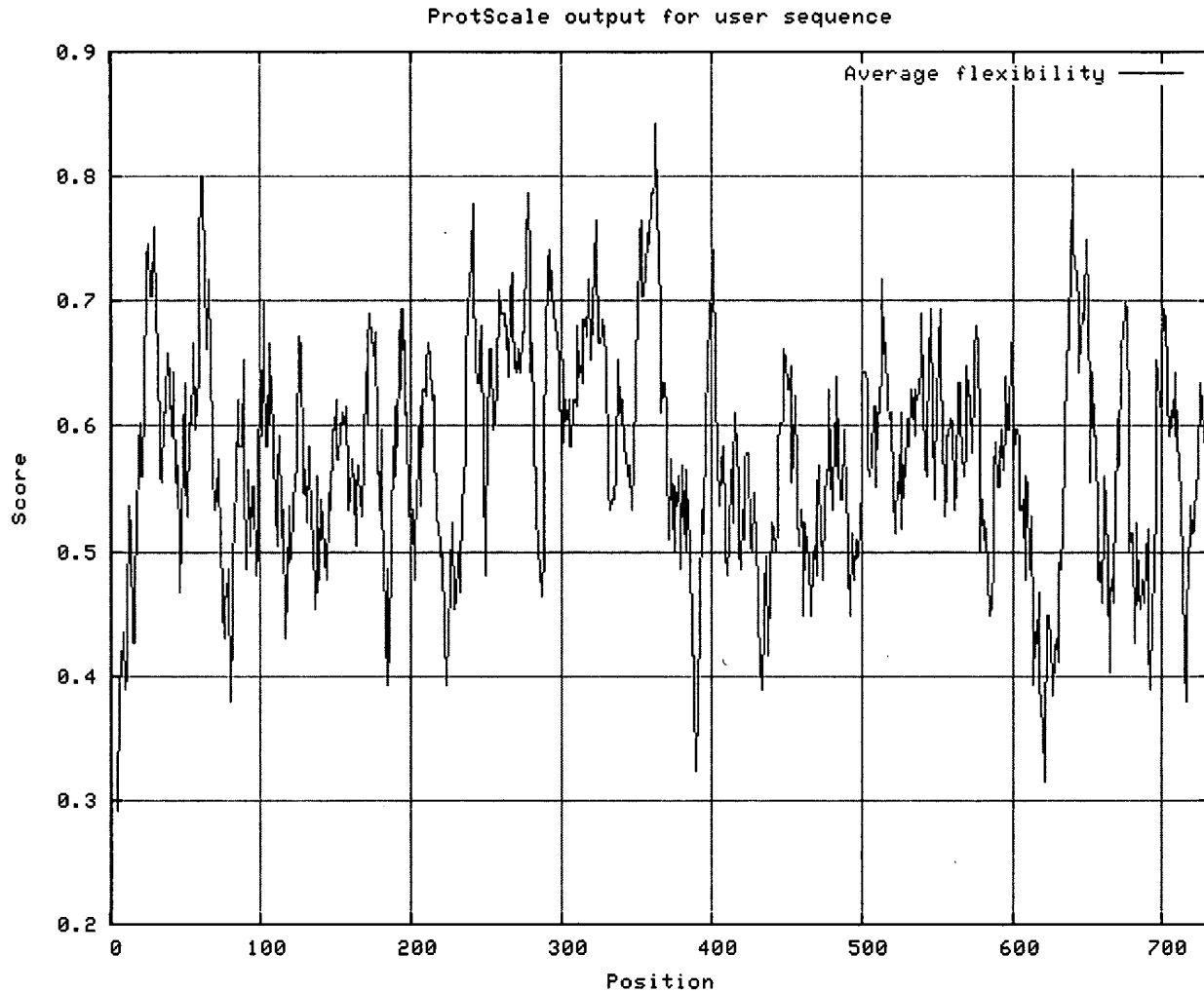


Figure 14B - 158P1D7 variant 3  
Average Flexibility Profile  
(Bhaskaran R., Ponnuswamy P.K., 1988.  
Int. J. Pept. Protein Res. 32:242-255)



## Figure 14c - 158P1D7 variant 4

### Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988.

Int. J. Pept. Protein Res. 32:242-255)

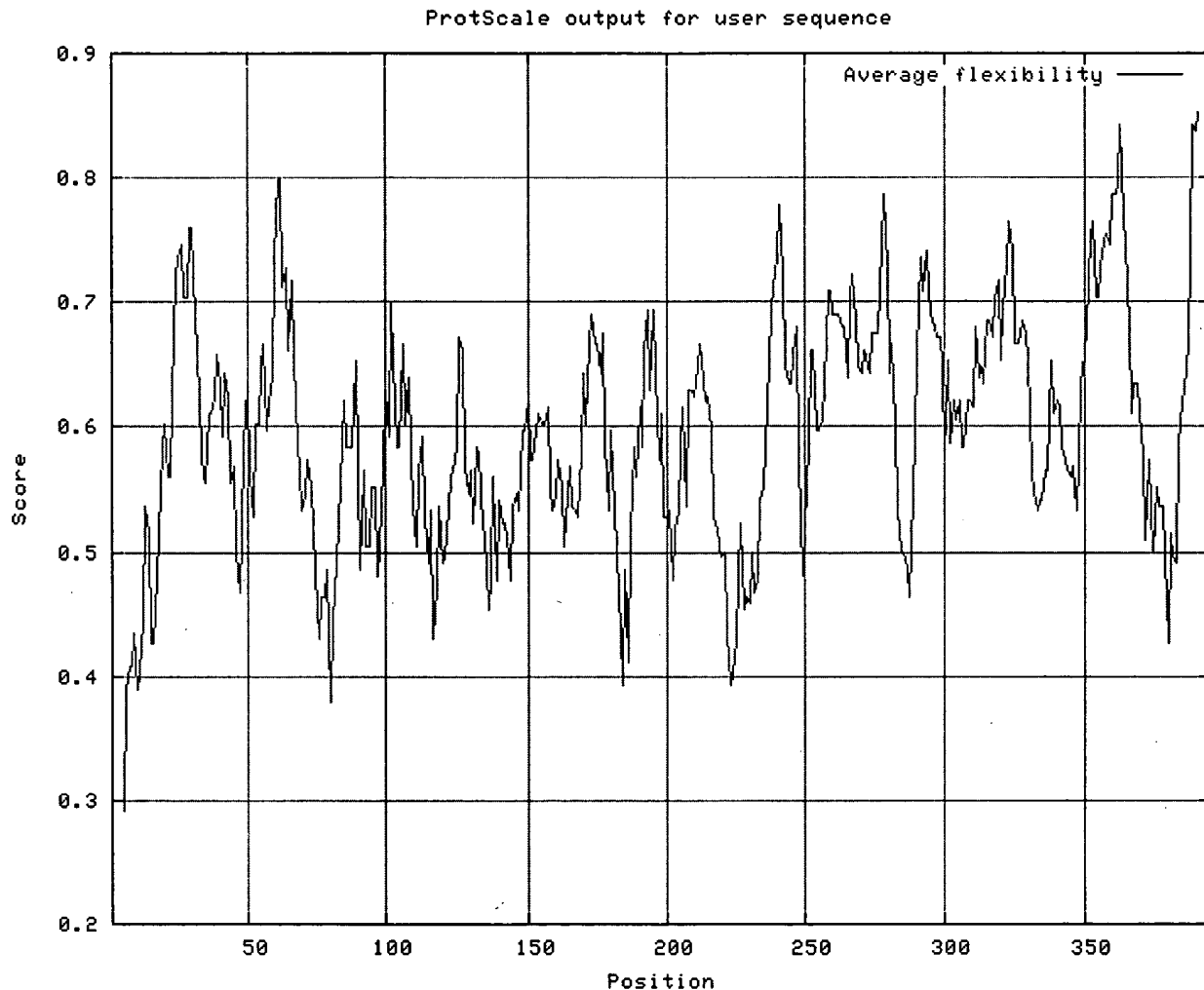




Figure 14d - 158P1D7 variant 6  
Average Flexibility Profile  
(Bhaskaran R., Ponnuswamy P.K., 1988.  
Int. J. Pept. Protein Res. 32:242-255)

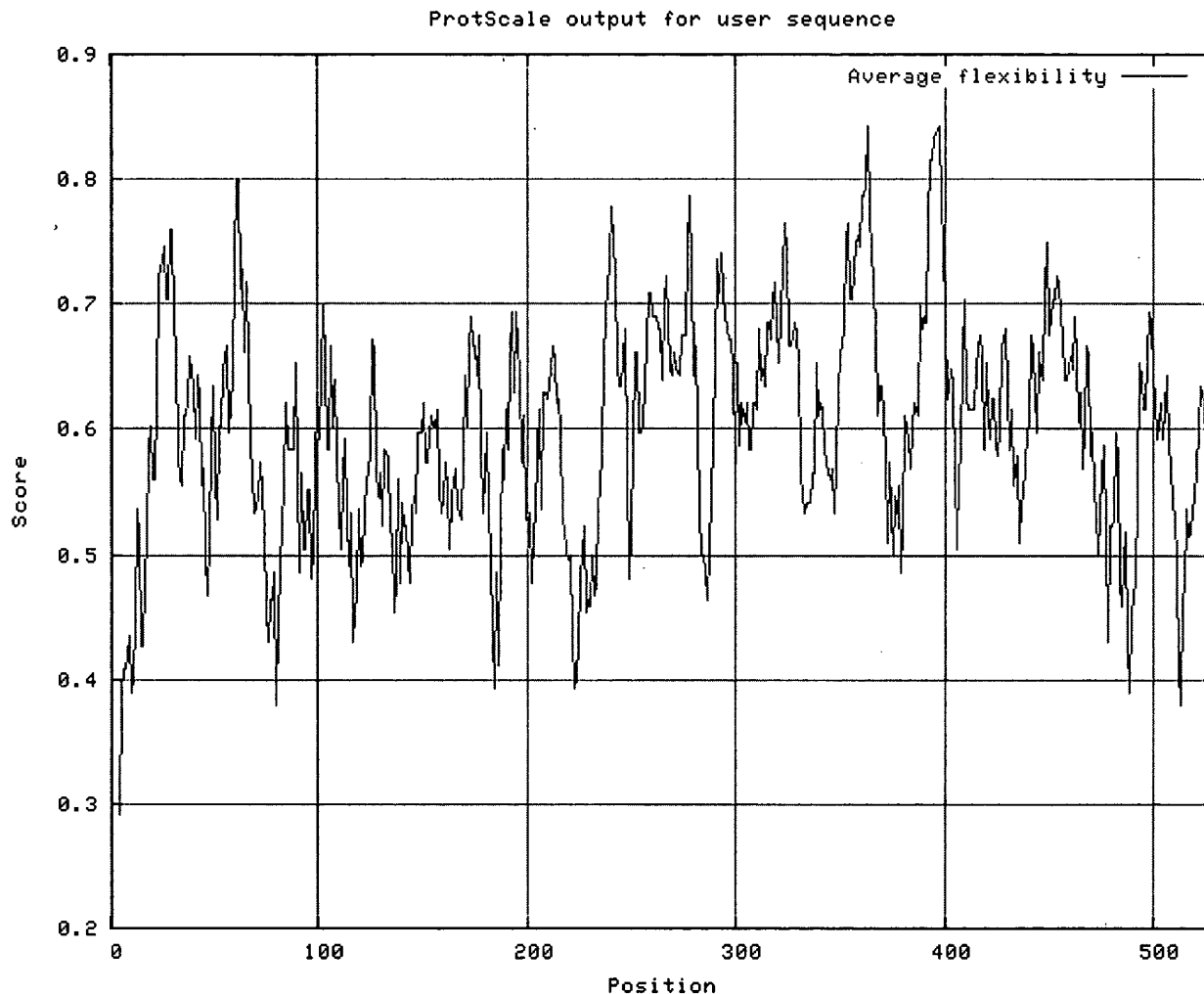
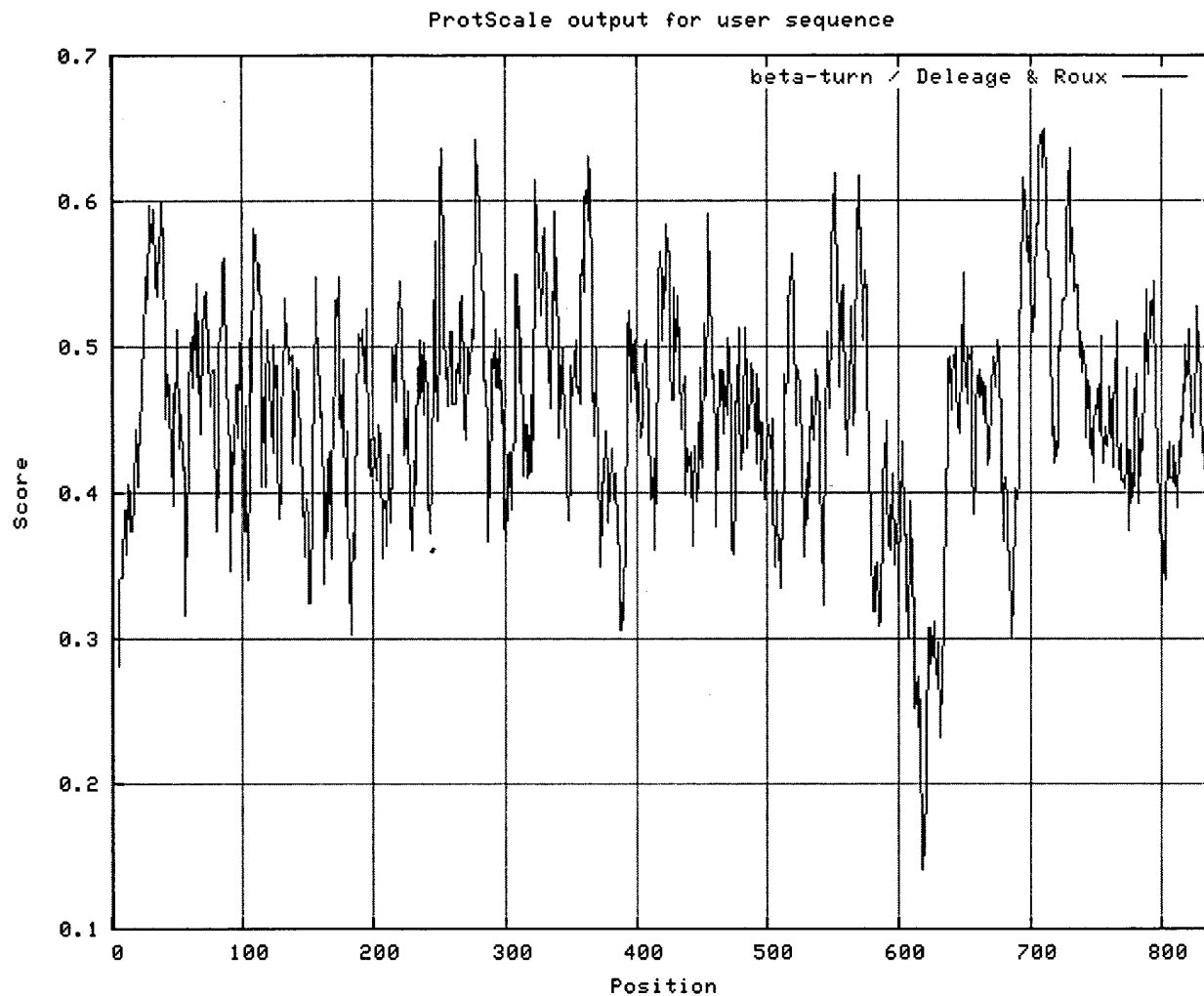


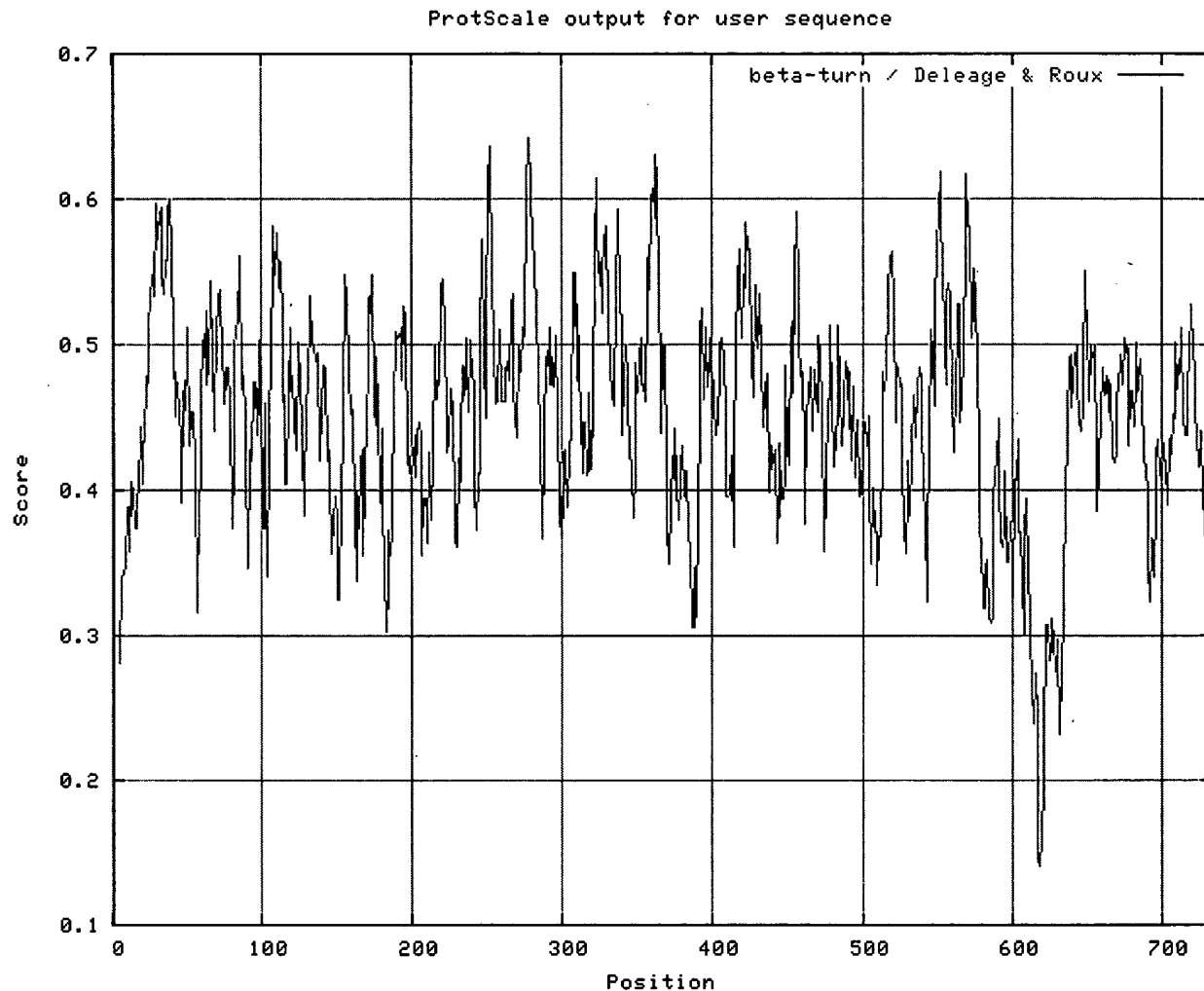
Figure 15a - 158P1D7  
variant 1 Beta-turn Profile  
(Deleage, G., Roux B. 1987.  
Protein Engineering 1:289-294)



## Figure 15b - 158P1D7 variant 3

### Beta-turn Profile

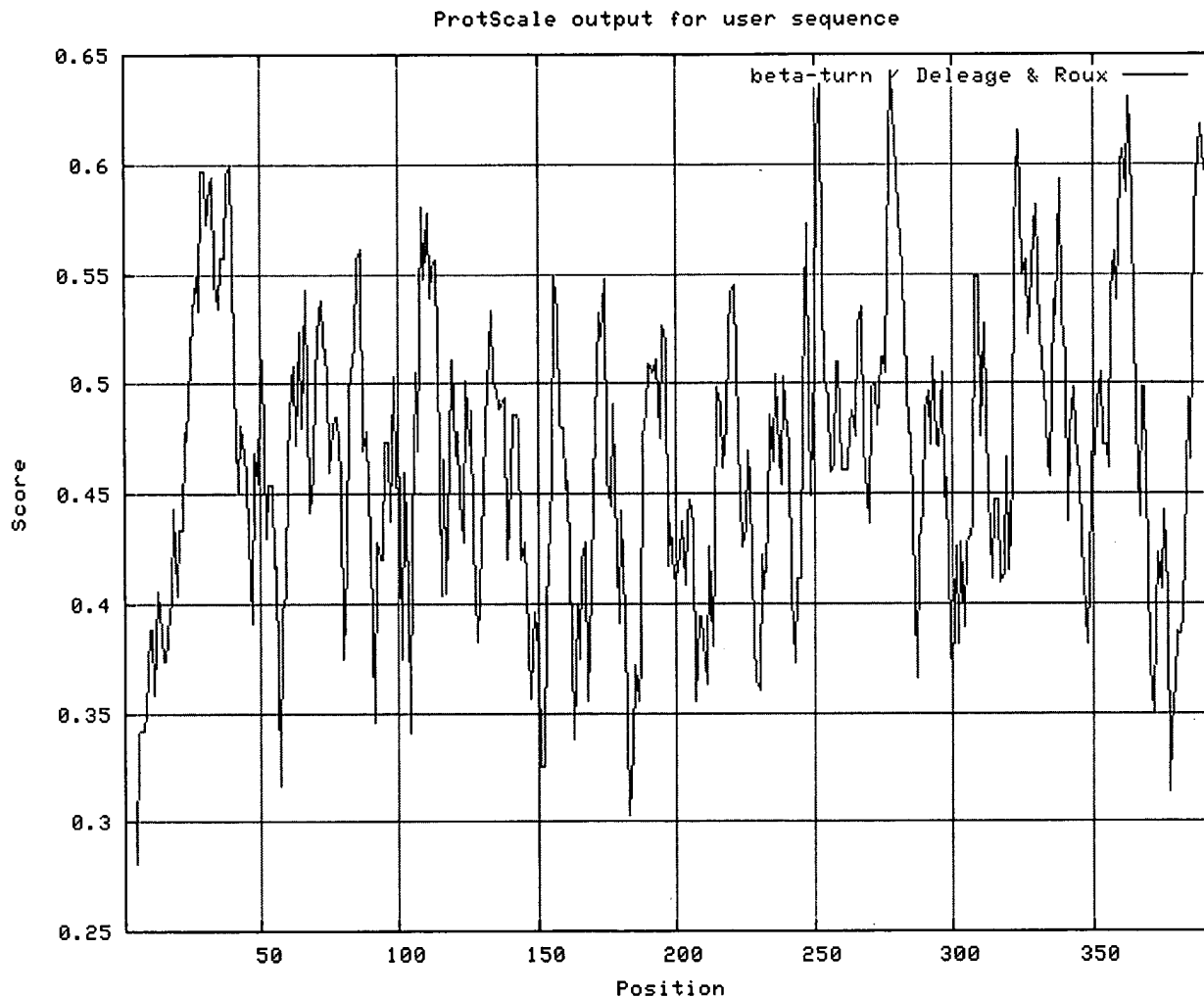
(Deleage, G., Roux B. 1987.  
Protein Engineering 1:289-294)



## Figure 15c - 158P1D7 variant 4

### Beta-turn Profile

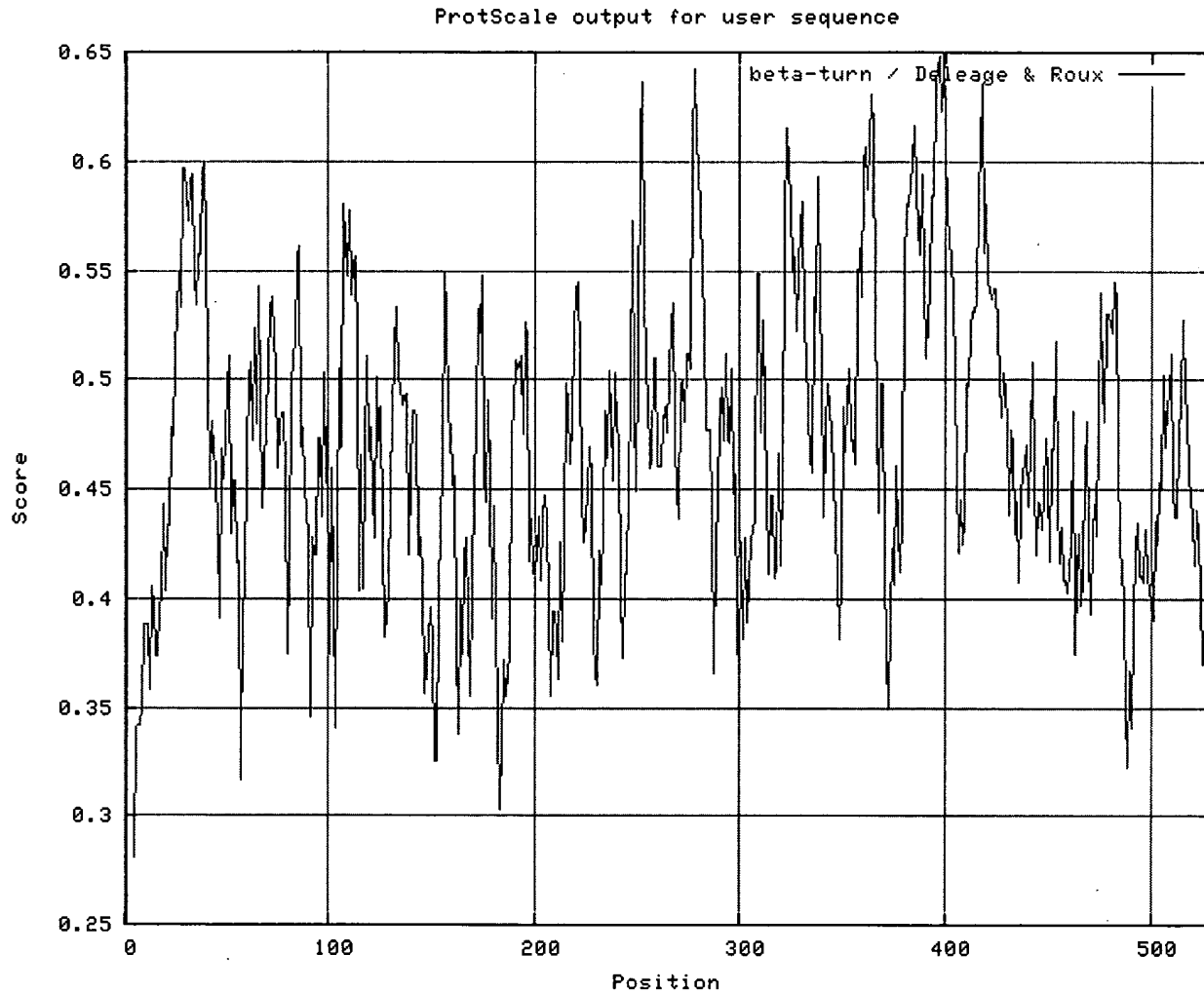
(Deleage, G., Roux B. 1987.  
Protein Engineering 1:289-294)



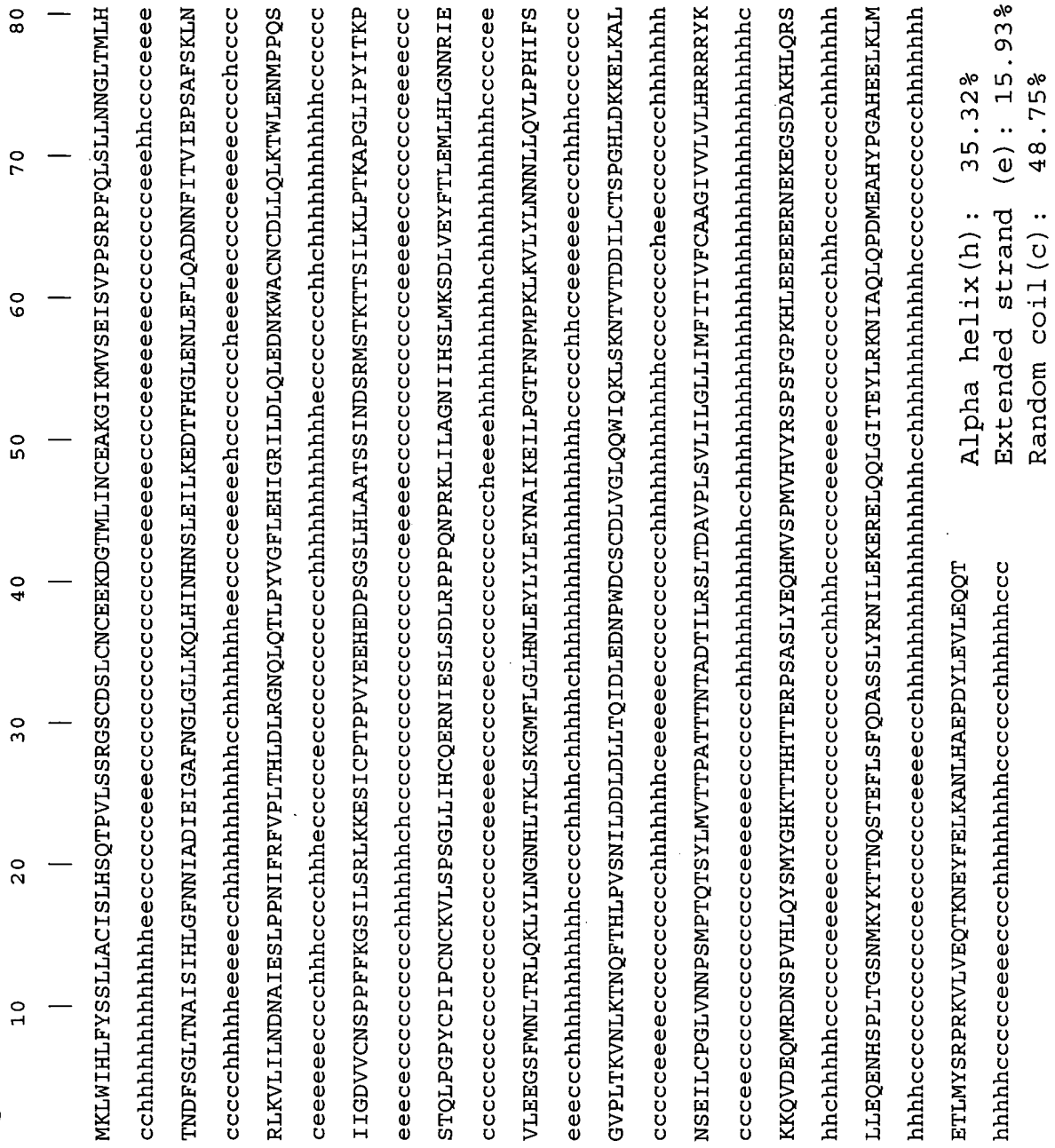
## Figure 15d - 158P1D7 variant 6

### Beta-turn Profile

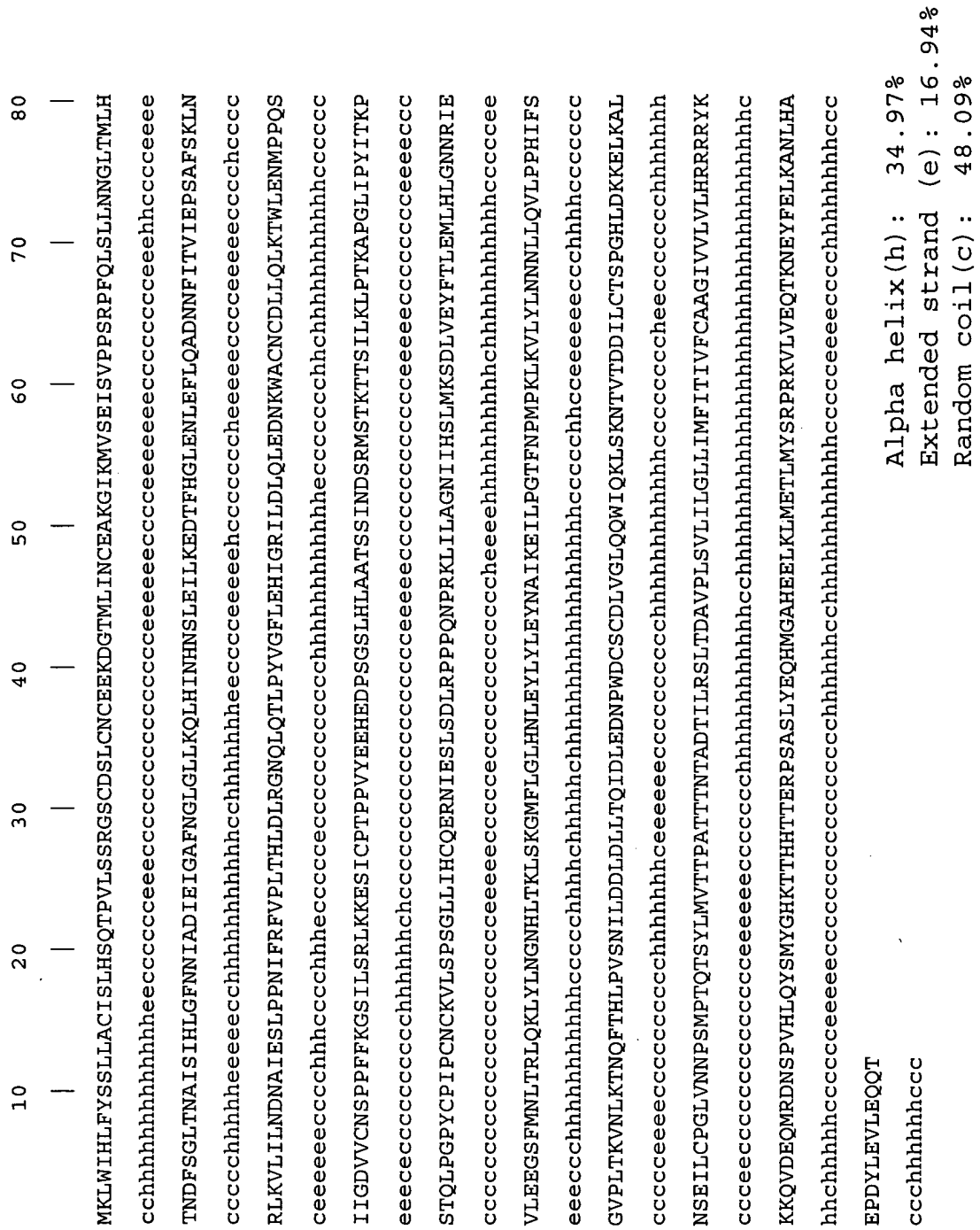
(Deleage, G., Roux B. 1987.  
Protein Engineering 1:289-294)



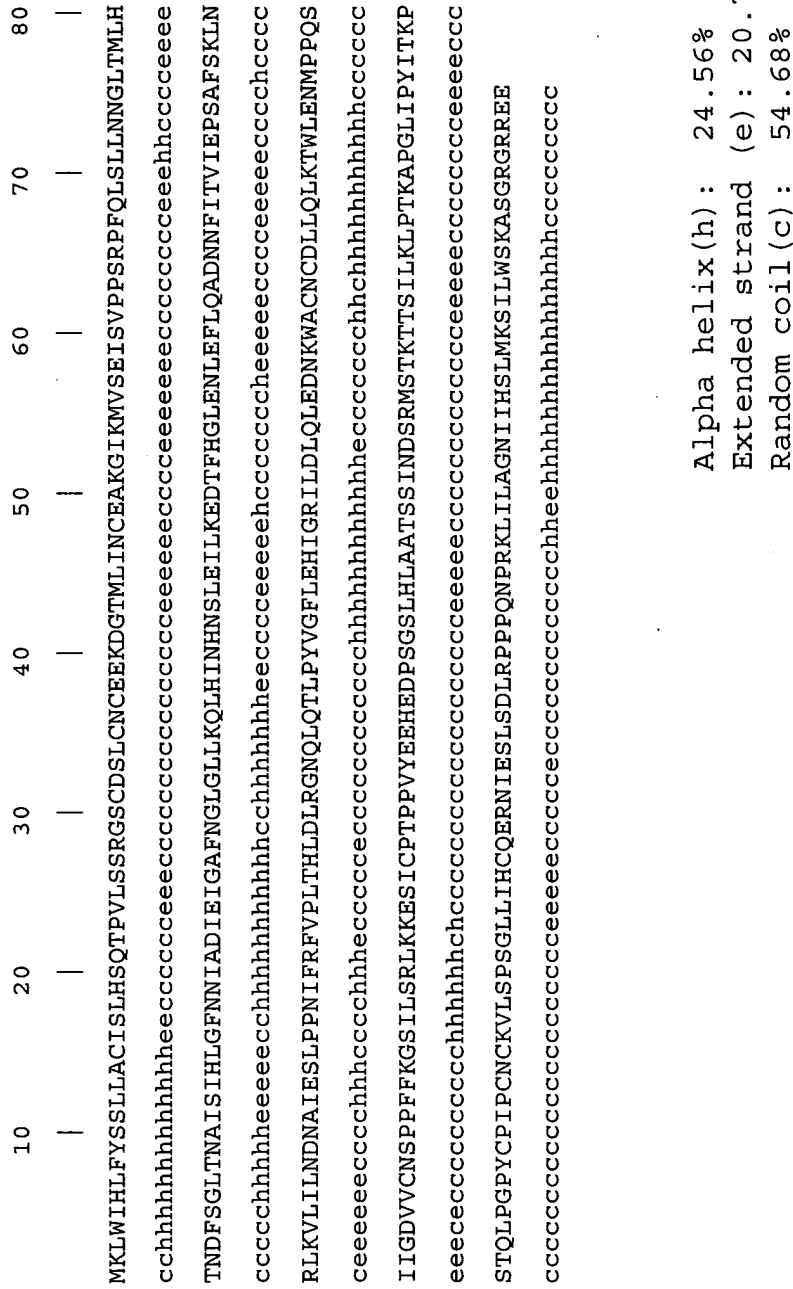
**Fig 16A** Secondary structure prediction of 158P1D7 variant 1



### Secondary structure prediction of 158P1D7 variant 3

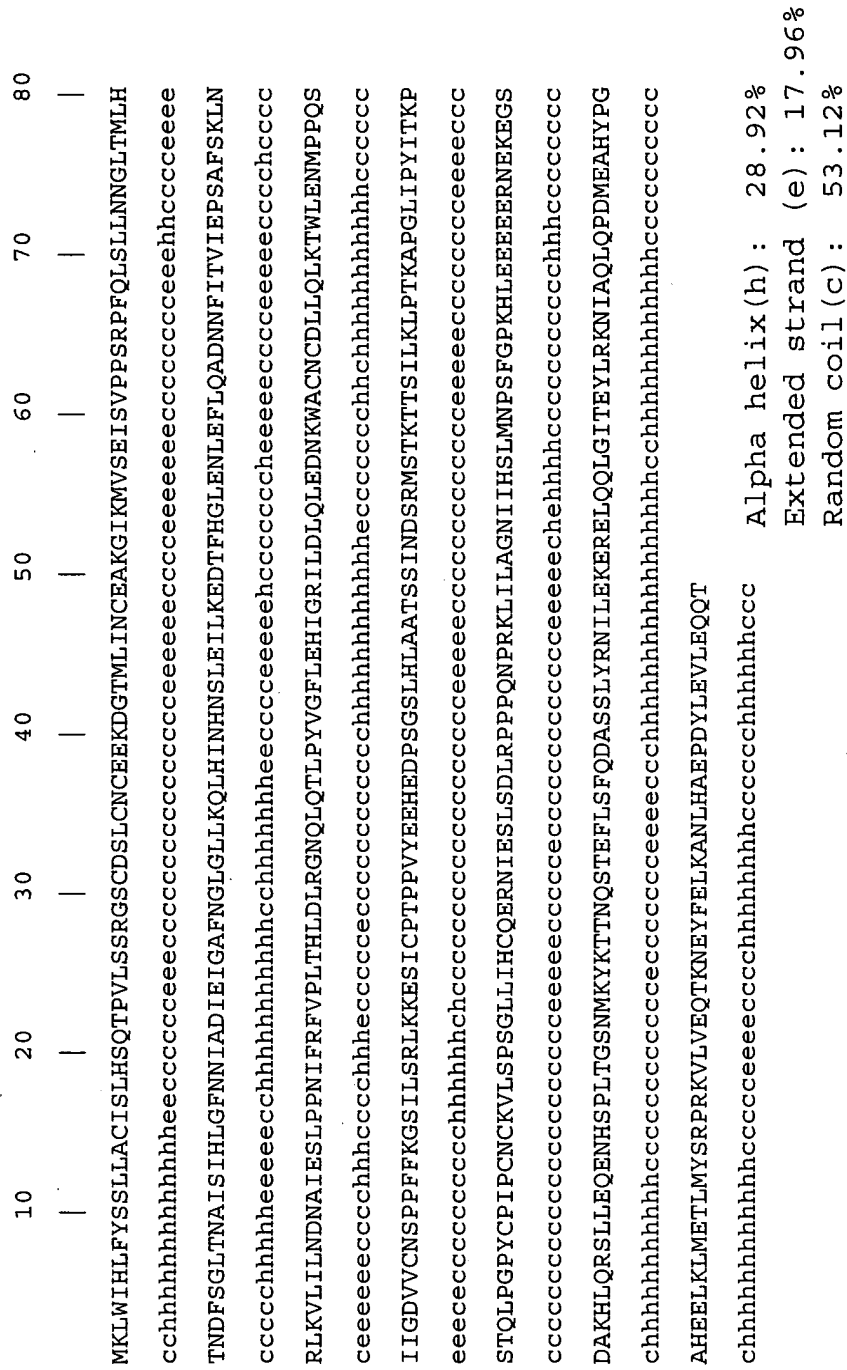


**Fig 16C**  
Secondary structure prediction of 158P1D7 variant 4



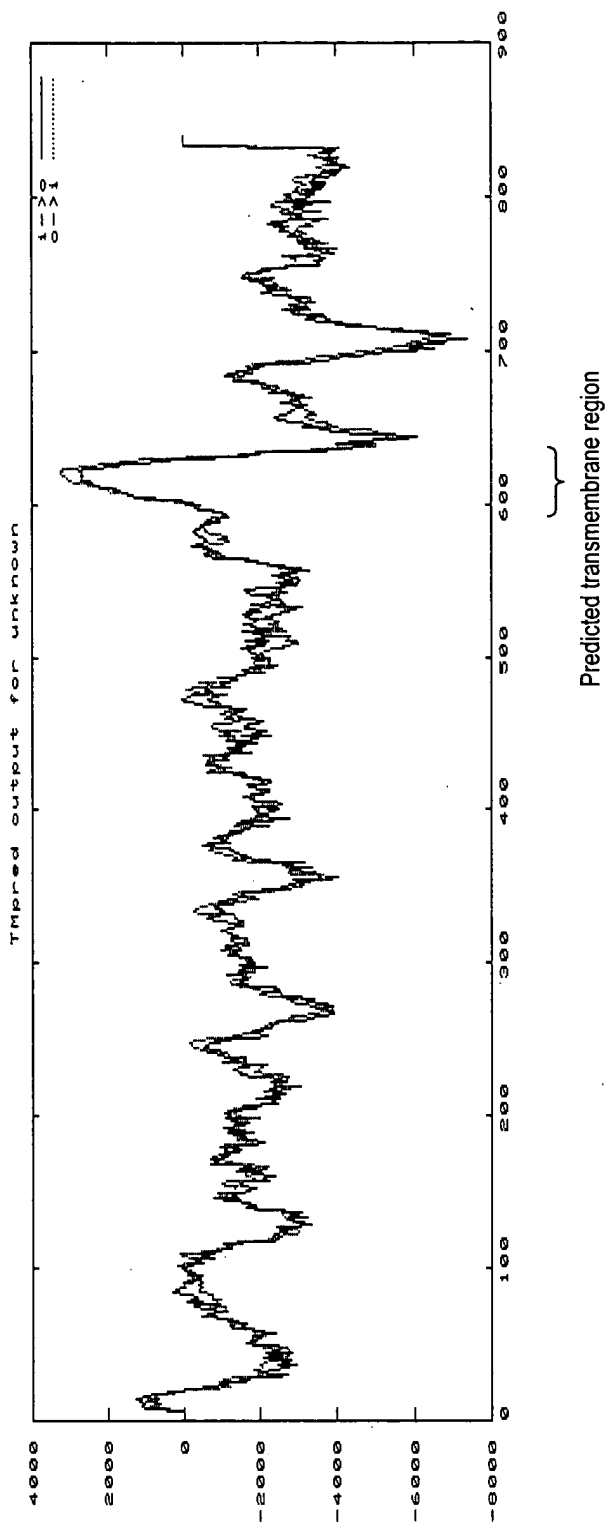


**Fig 16D**  
Secondary structure prediction of 158P1D7 variant 6



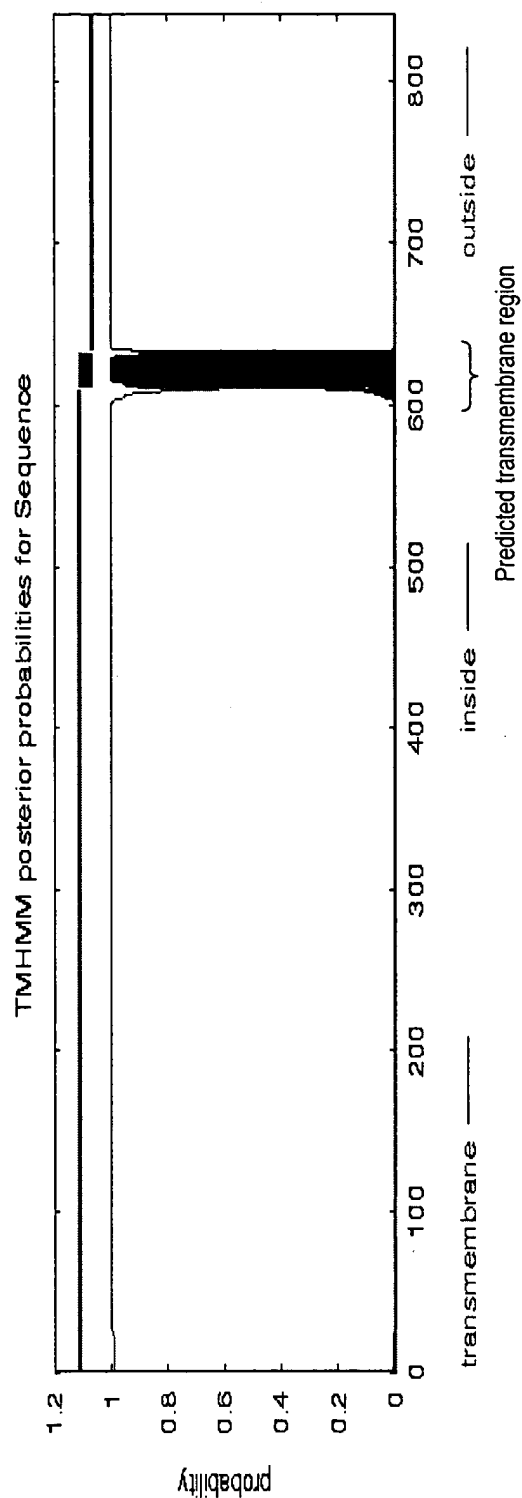
**Fig 16E**

**Transmembrane prediction for 158P1D7 variant 1**



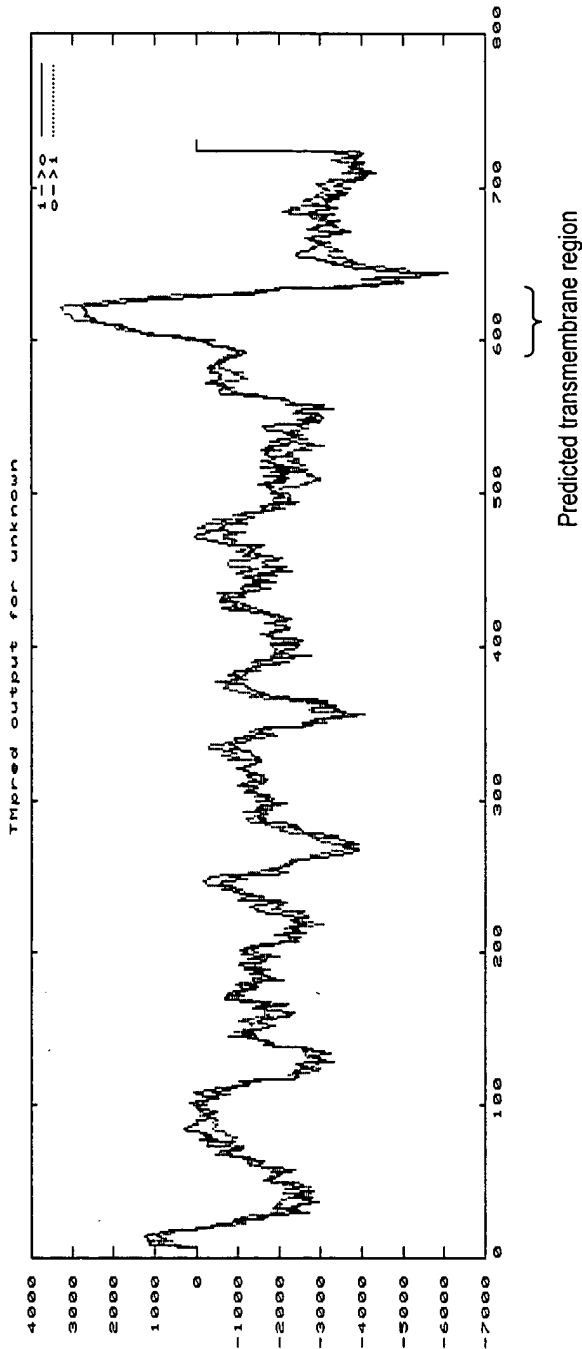
1 transmembrane  
domain  
predicted

**Fig 16F**



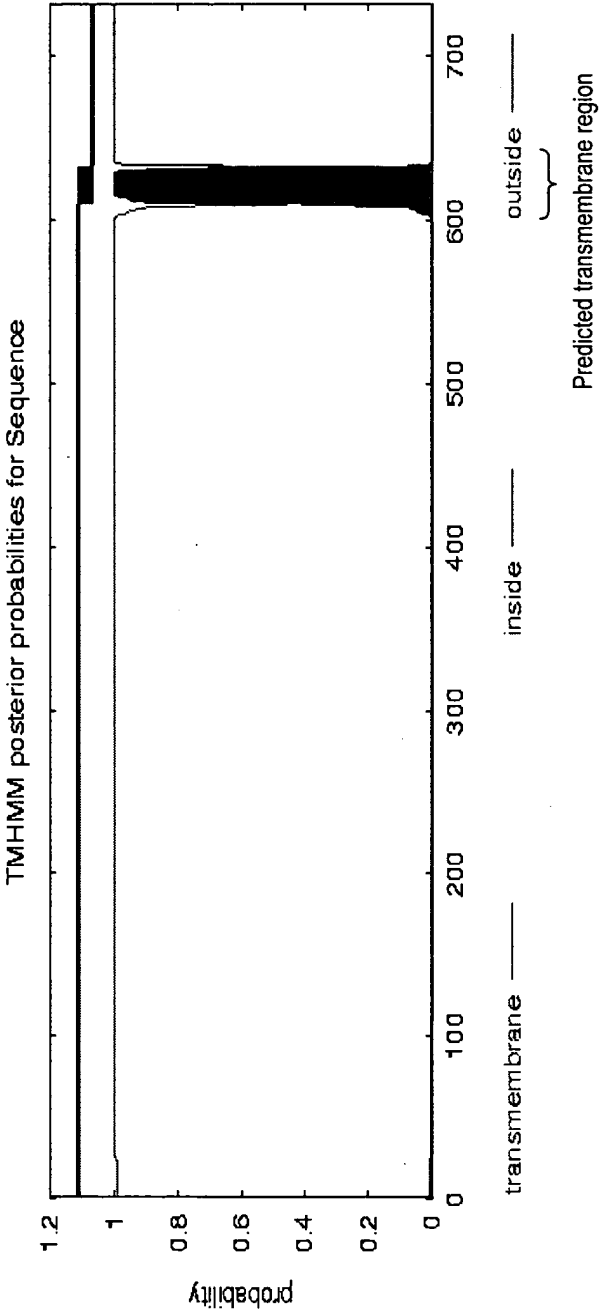
1 transmembrane  
domain  
predicted

Transmembrane prediction for 158P1D7 variant 3



1 transmembrane  
domain  
predicted

Fig 16H



1 transmembrane  
domain  
predicted

Fig 16I

Transmembrane prediction for 158P1D7 variant 4

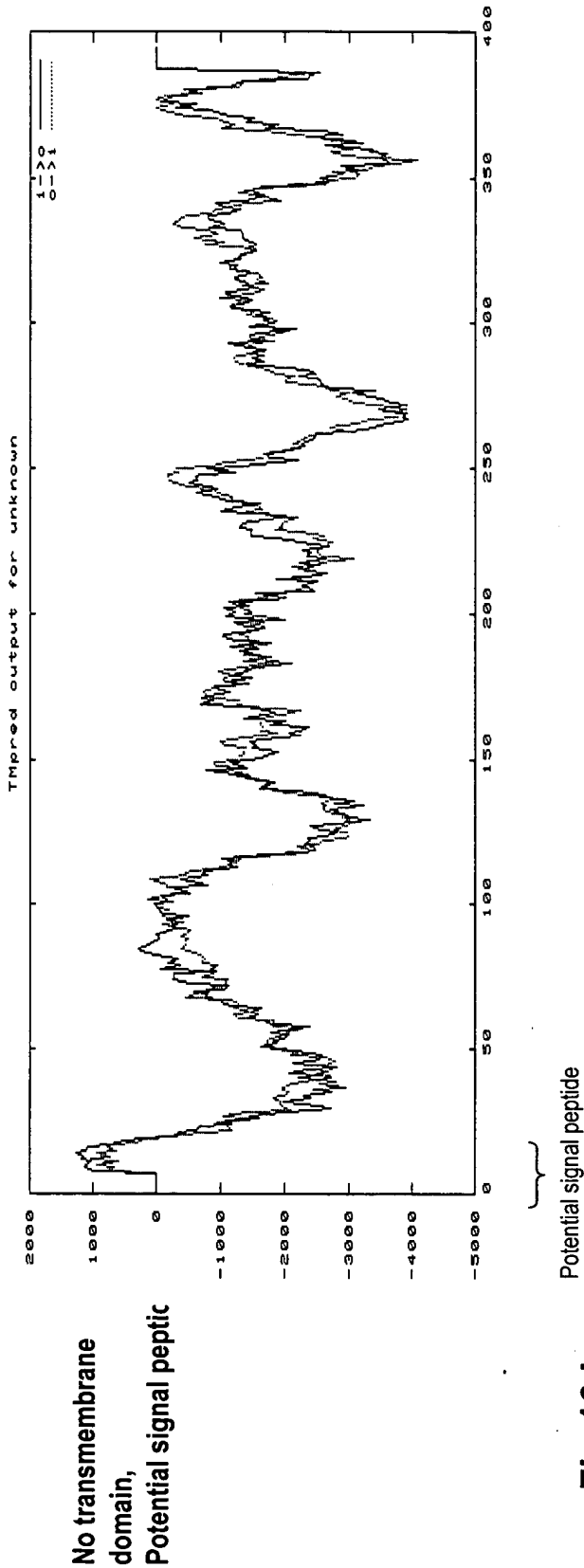


Fig 16J

TMHMM posterior probabilities for Sequence

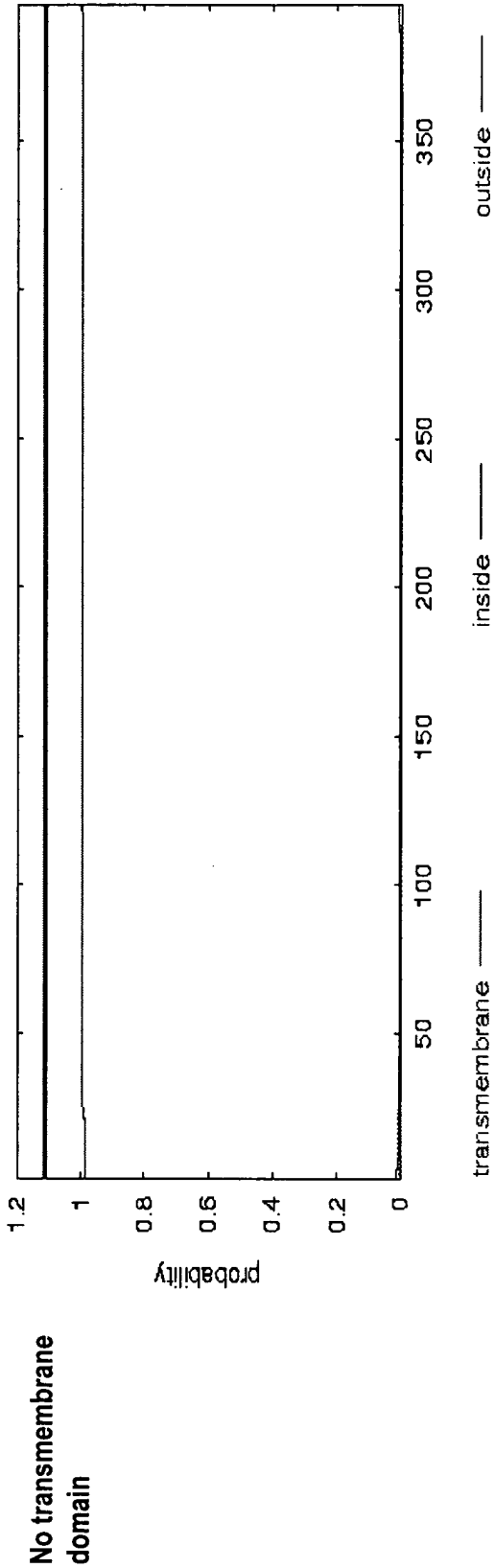
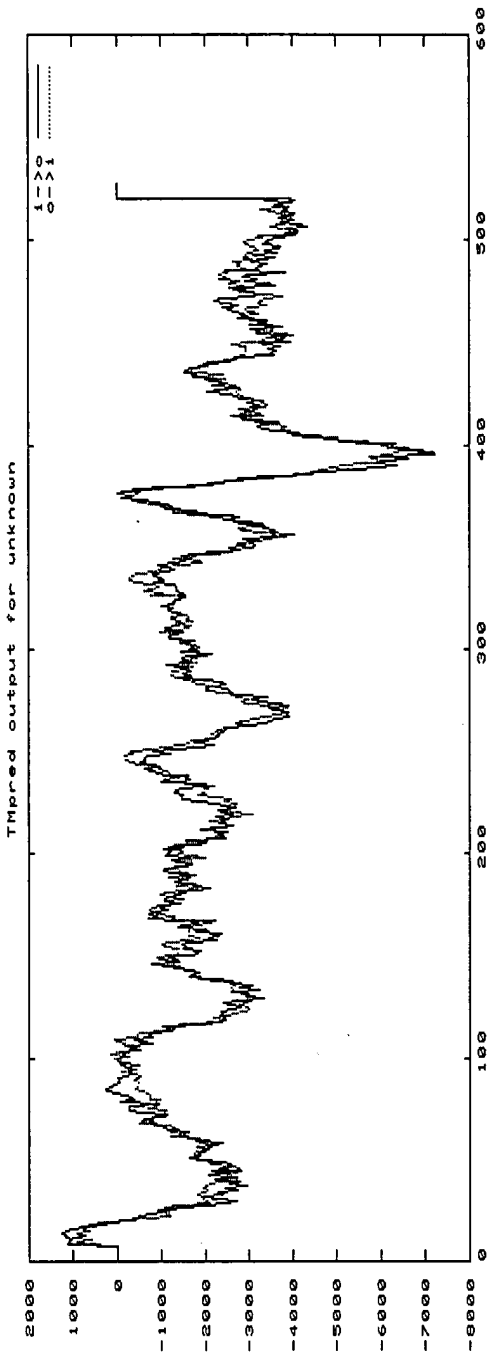


Fig 16K

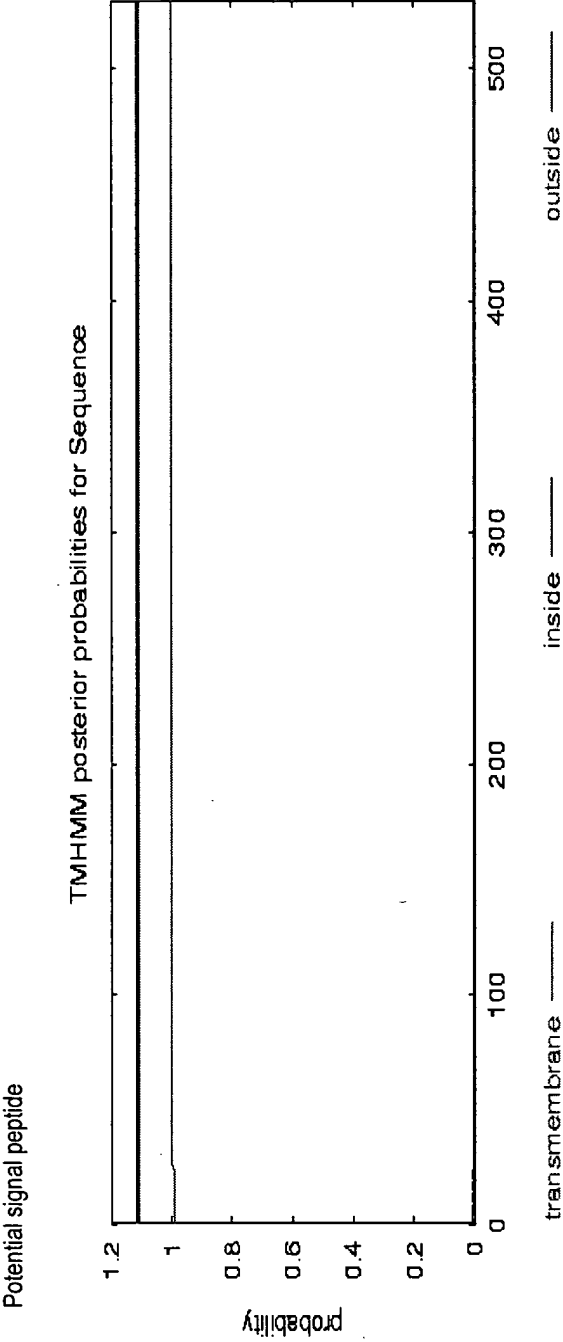
Transmembrane prediction for 158P1D7 variant 6



No transmembrane  
domain,  
Potential signal peptide

Fig 16L

TMHMM posterior probabilities for Sequence



No transmembrane  
domain

## Figure 17



**Figure 18**

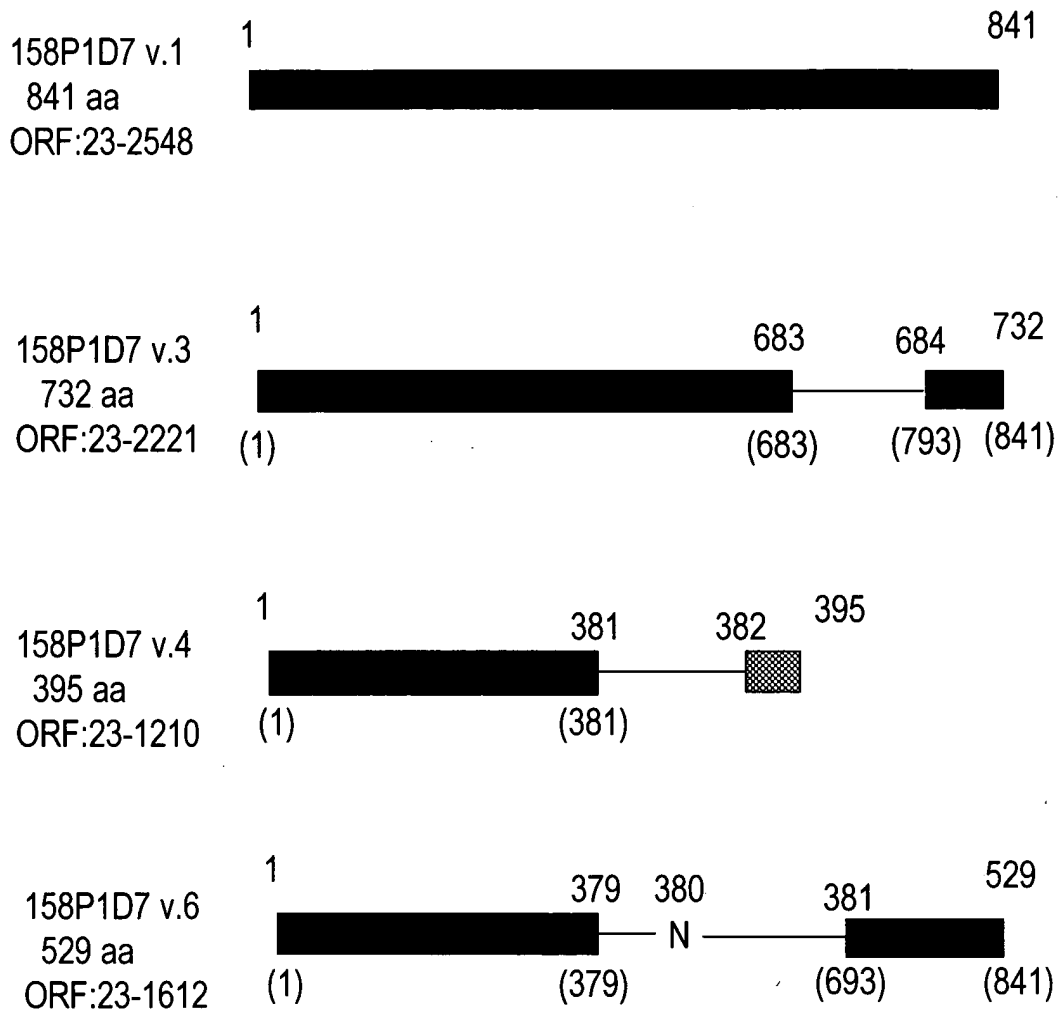
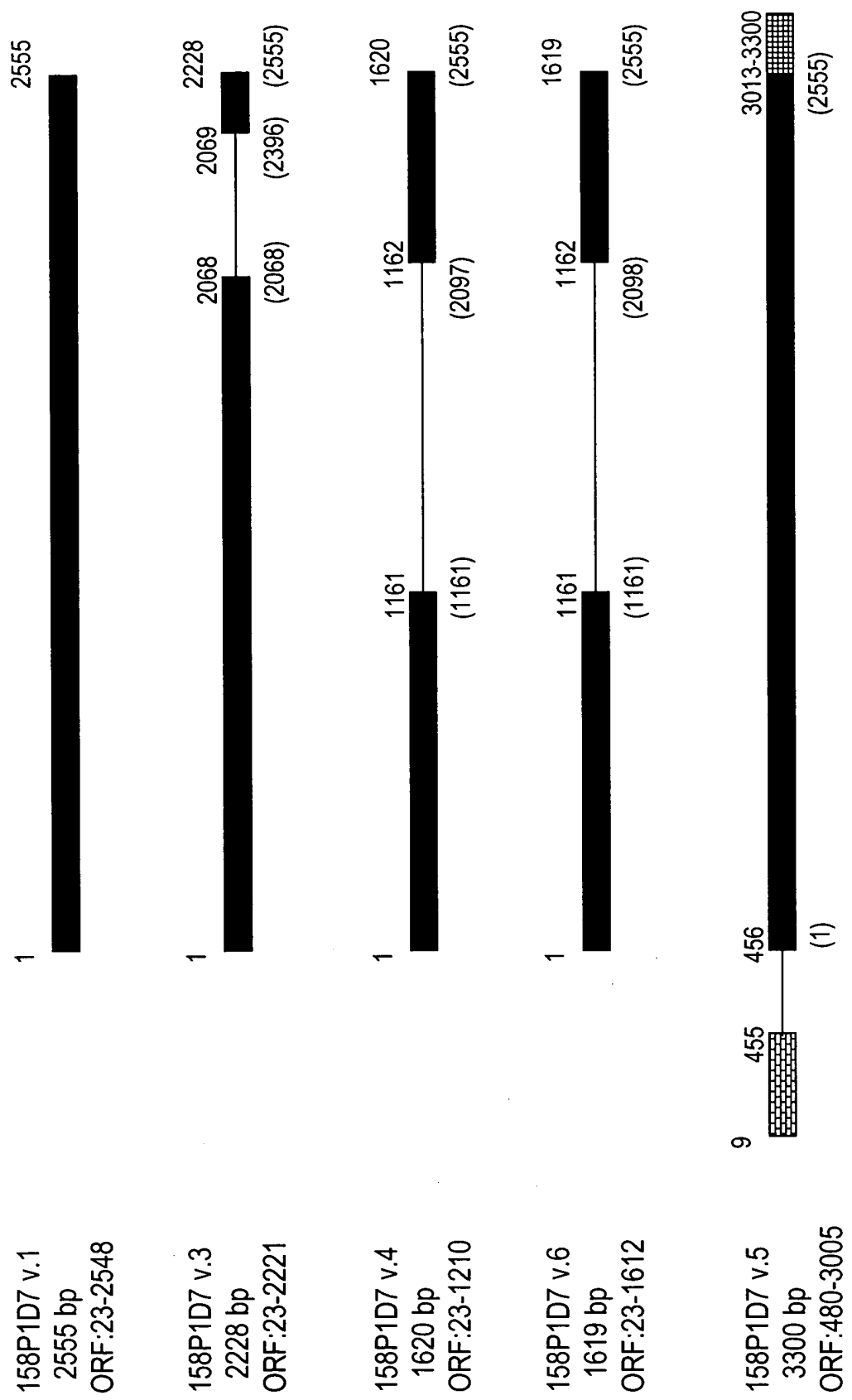


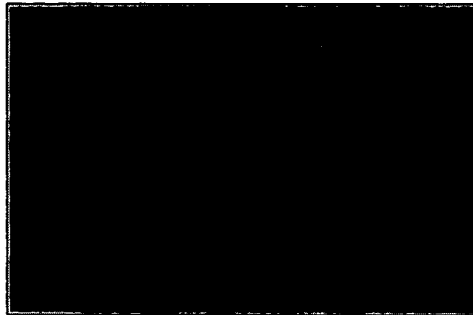
Figure 19





## Figure 20 158P1D7 Expression in Melanoma

1 2



1. Normal skin cell line - Detroit-551
2. Melanoma cancer cell line -- A375

**Figure 21 158P1D7 Expression in Cervical  
Cancer Patient Specimens**

Panel#	Patient ID#	Diagnosis	Grade	Stage	Cervix CA
1	Normal Cervix	(Ambion)			
2	HeLa	Cell Line			
3	USA-00281-D01	Intraepithelial neoplasia	2-3	T3AN0MX	
4	VNM-00266	AdenoCA	1	IIA	
5	VNM-00376	AdenoCA	1	IIA	
6	IND-00396	Mucinous AdenoCA	2	IIB	
7	A0098	Adenosquamous	2B	T2bNXM0	

No expression

Positive expression



Figure 22: Detection of AGS15 protein in recombinant cells  
 with monoclonal antibodies

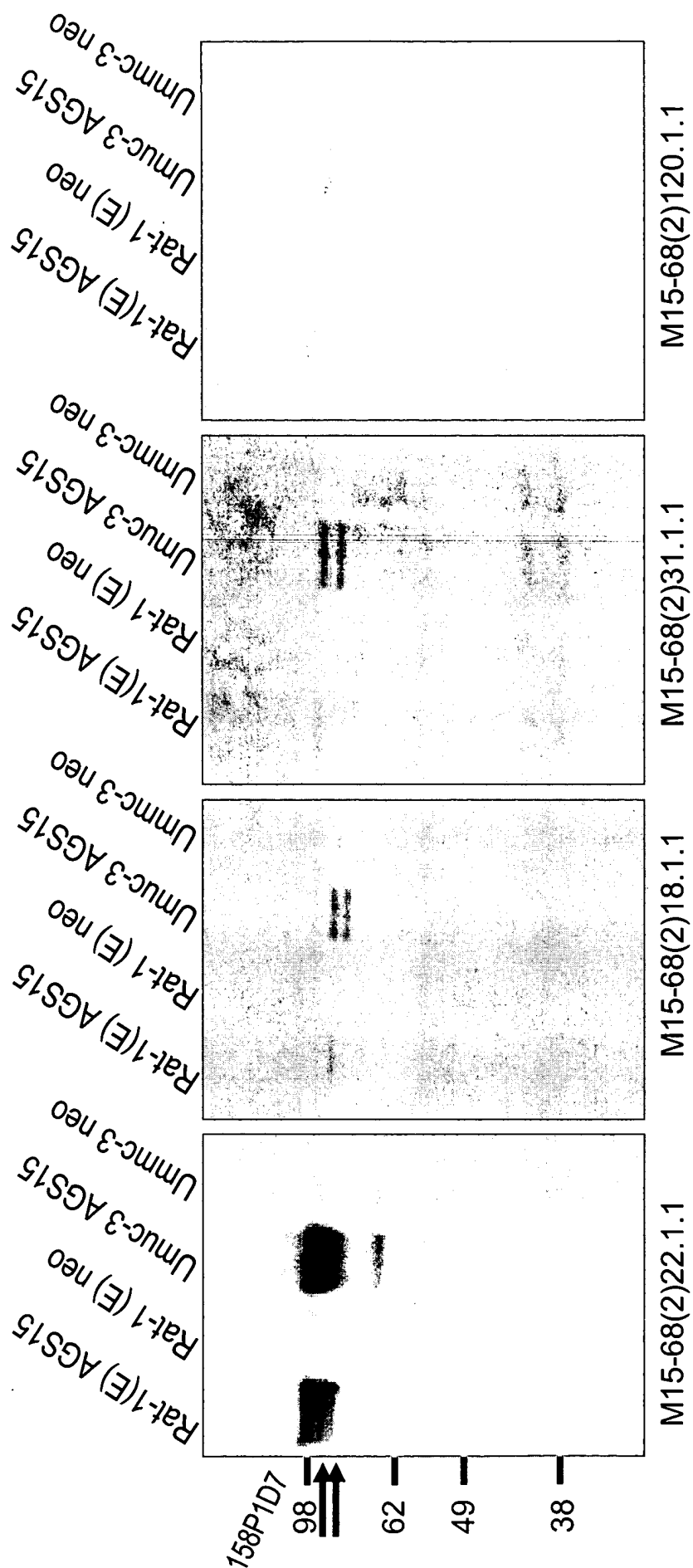


Figure 23: Surface staining of AGS15-expressing 293T and UMUC cells  
 with anti-AGS15 monoclonal antibodies

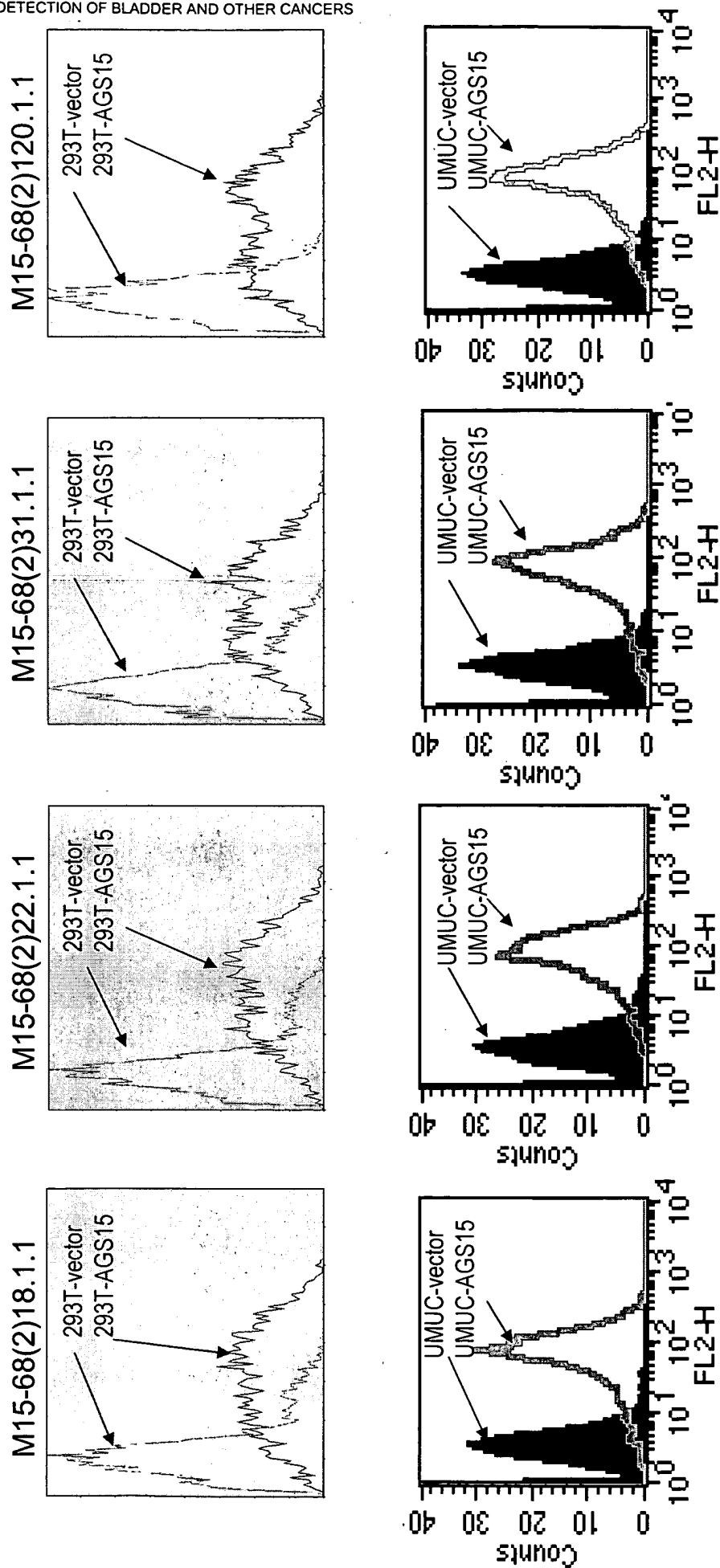
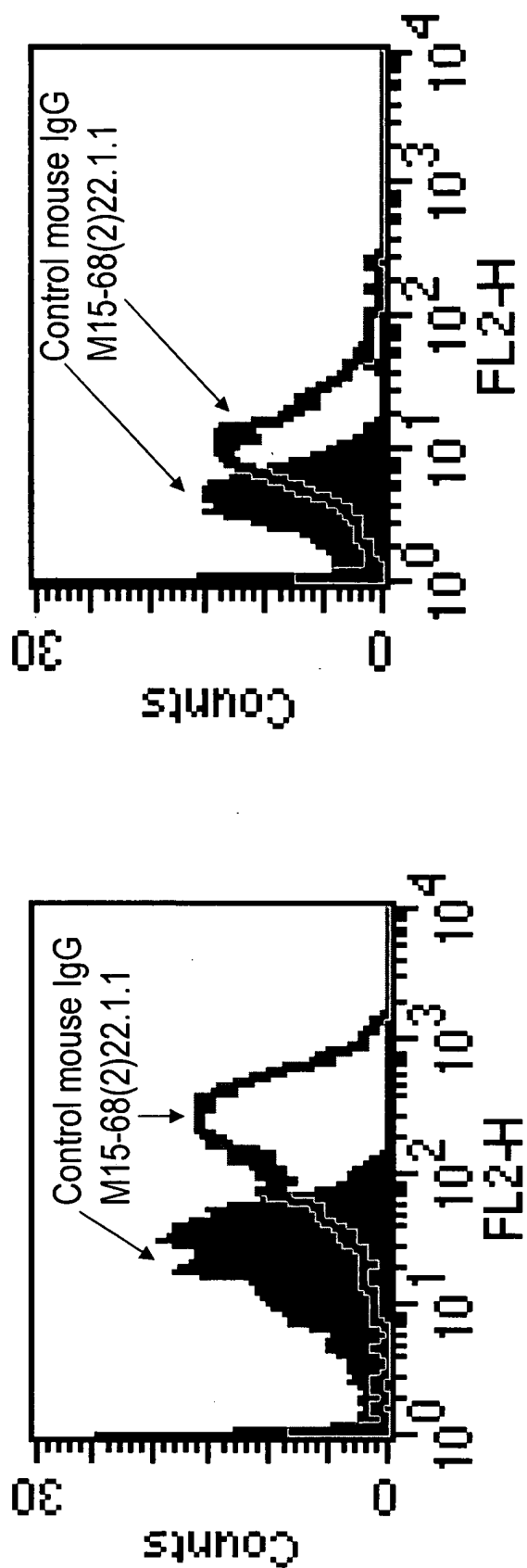


Figure 24: Surface staining of endogenous AGS15-expressing LAPC9 prostate cancer and UGB1 bladder cancer xenograft cells with MAb M15-68(2)22.1.1



**Figure 25: Monoclonal antibody-mediated internalization of endogenous surface 158P1D7 in NCI-H146 small cell lung cancer cells**

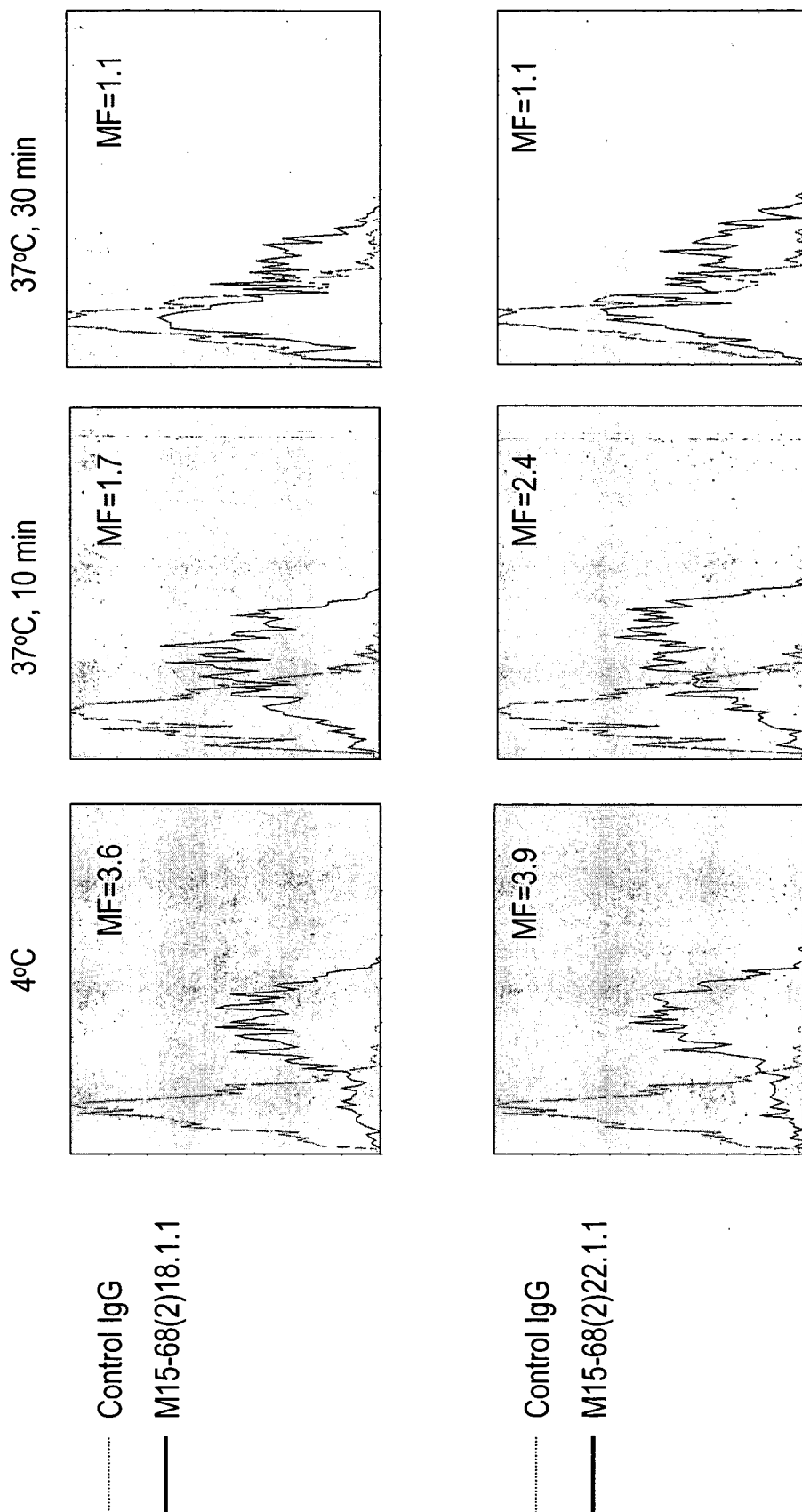
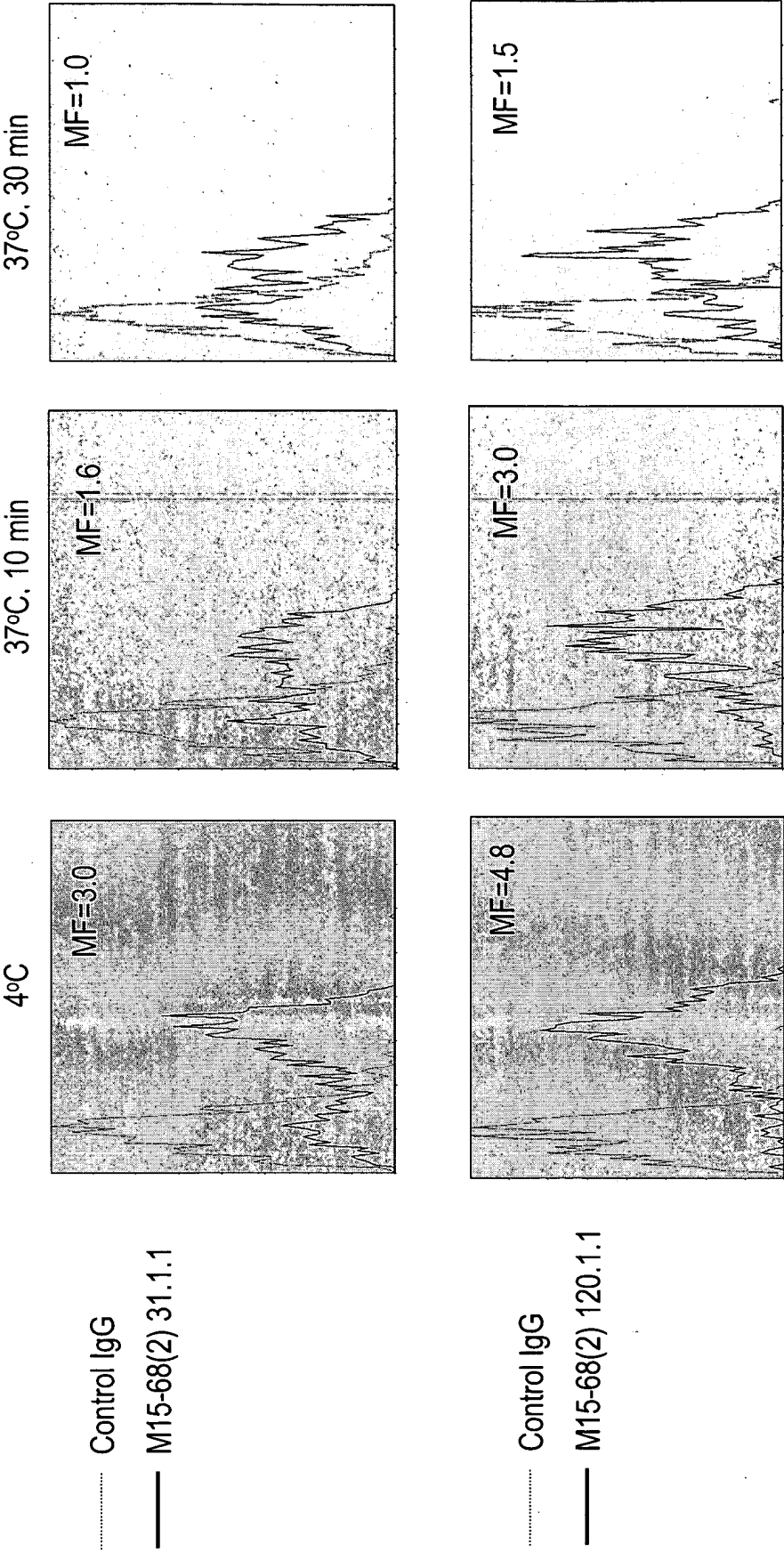
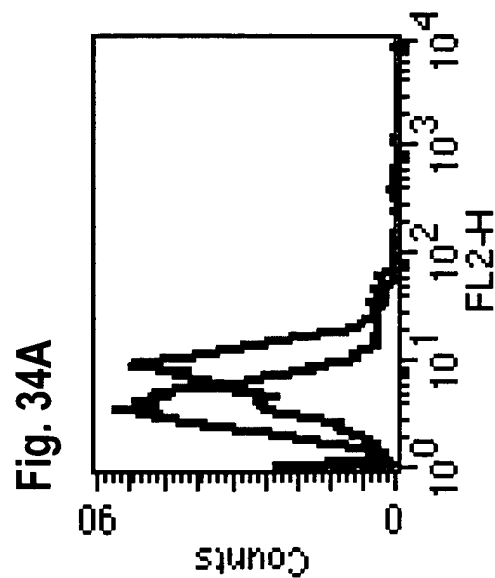


Figure 25 Cont.



**Figure 26: Binding of the 158P1D7 extracellular domain to human umbilical vein endothelial cells (HUVEC)**



Key	Name	Parameter	Gate
—	HUVEC No ECD / anti-158P1D7-PE	FL2-H	G1
—	HUVEC 158P1D7 ECD / anti-158P1D7-PE	FL2-H	G1

2.88% vs 6.53% gated

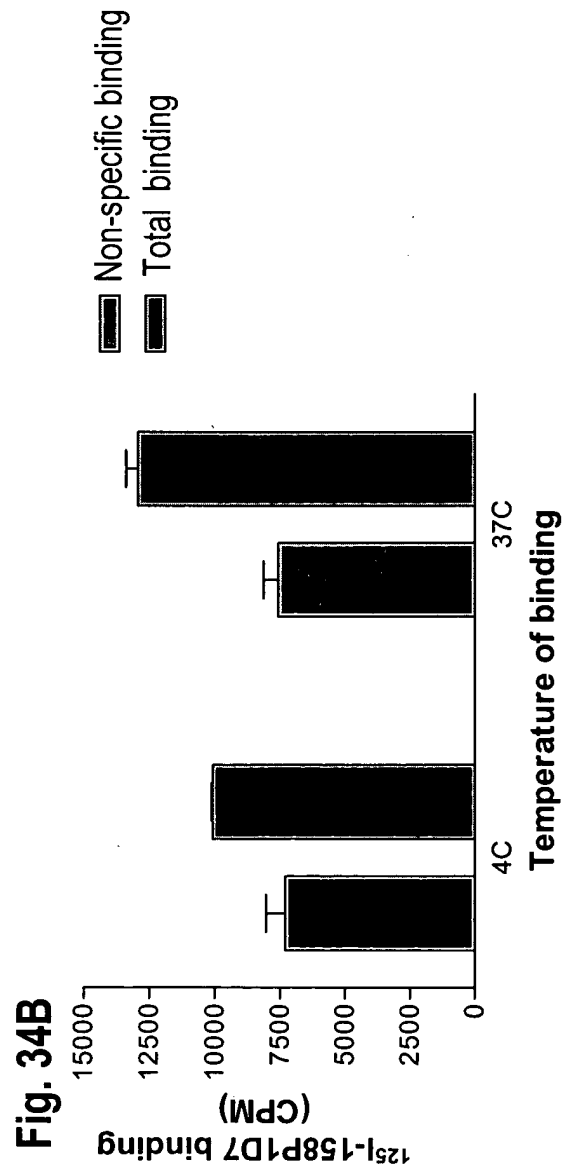




Figure 27 - 158P1D7 Enhances the Growth of Bladder Cancer UM-UC-3 Cells in Mice

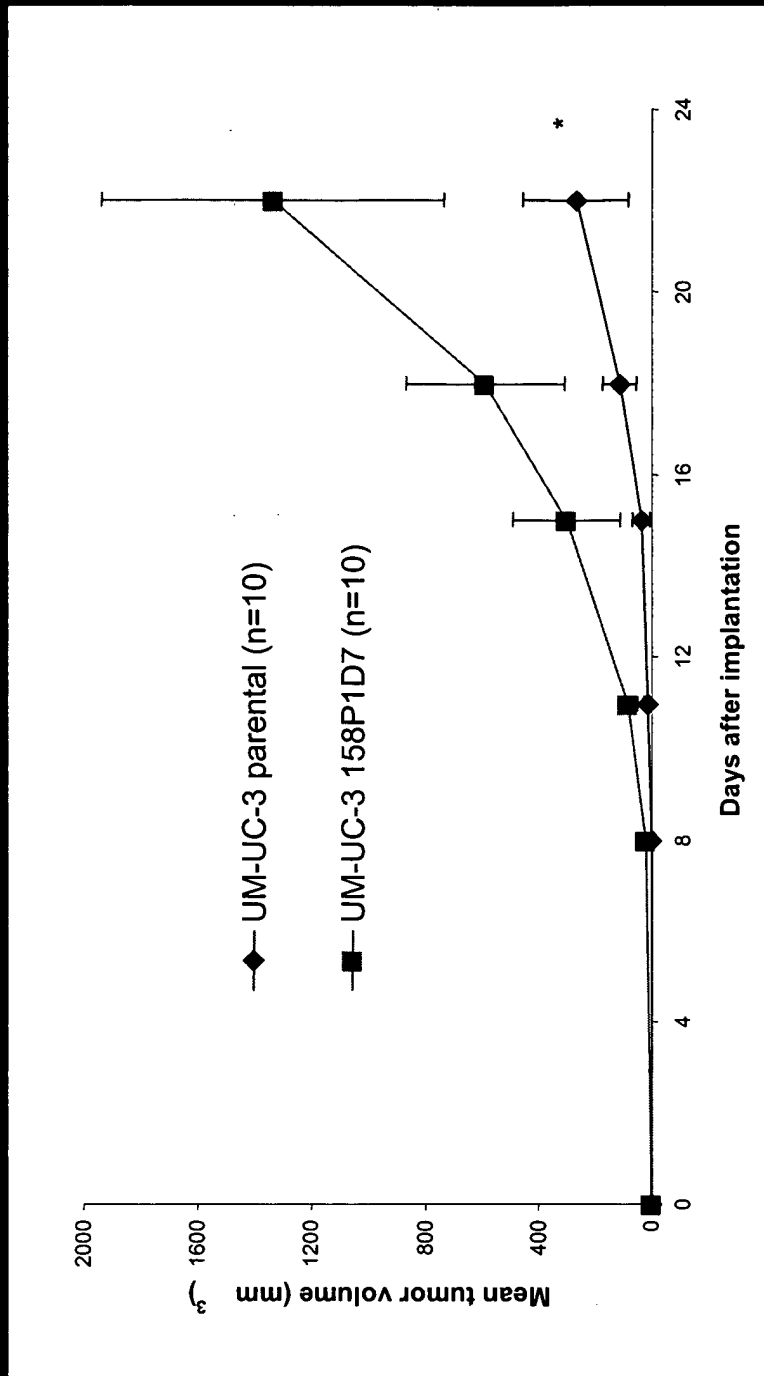
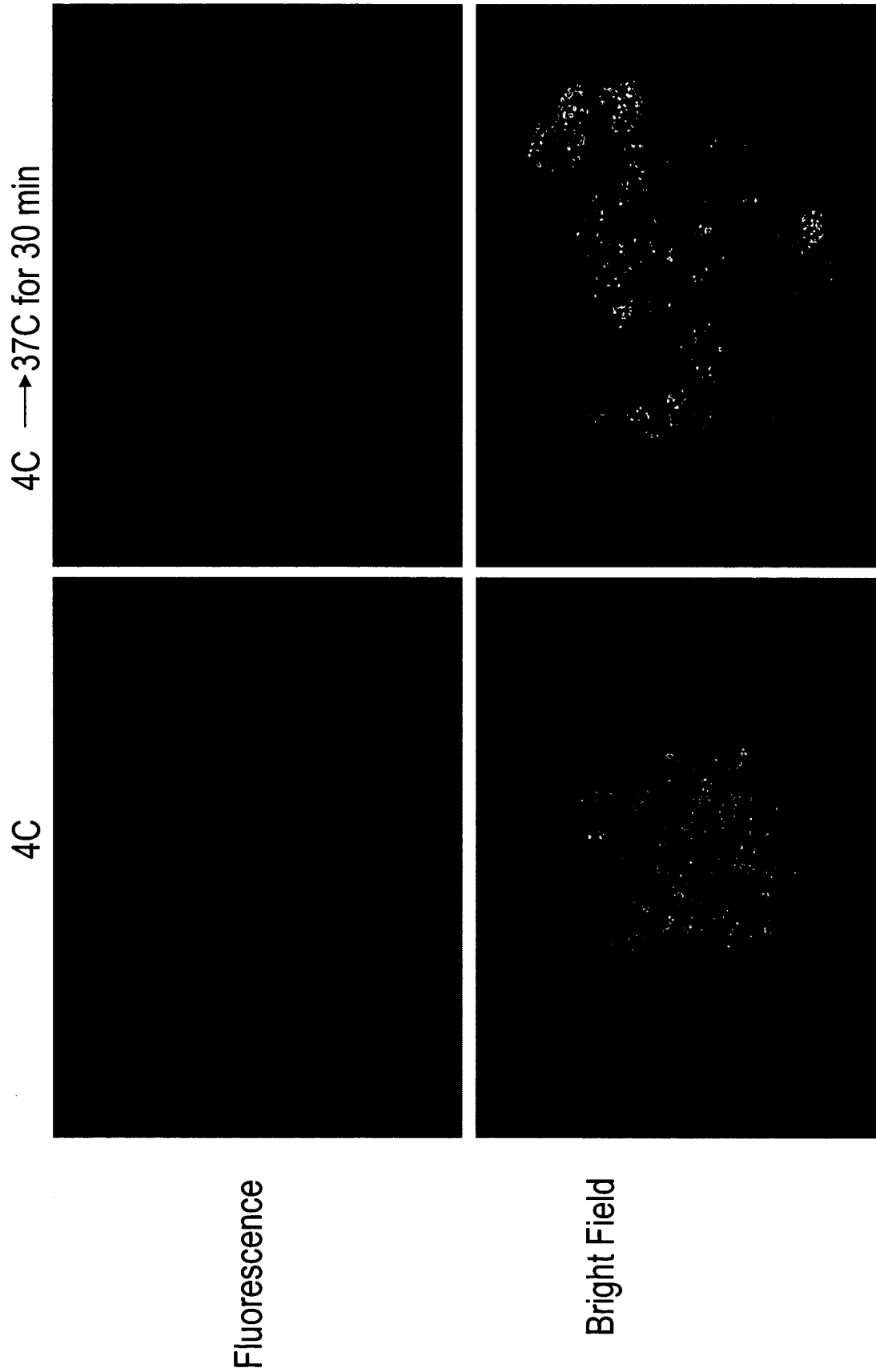


Figure 28: Internalization of MAbs M15-68(2).31.1.1 in NCI-H146 cells



**Figure 29: Effect of 158P1D7 RNAi on cell survival**

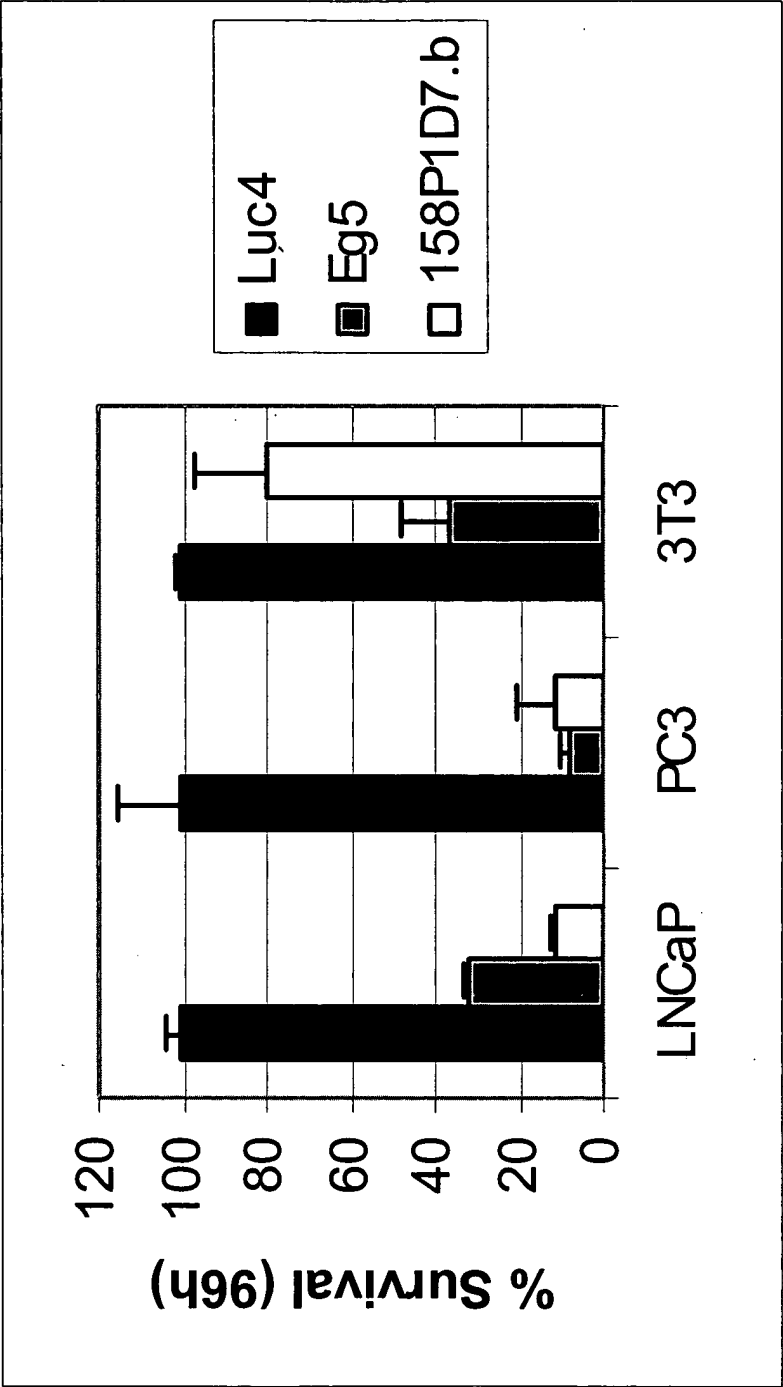


Figure 30 - 158P1D7 MAbs Retard the Growth of Human Bladder Cancer Xenografts in Mice

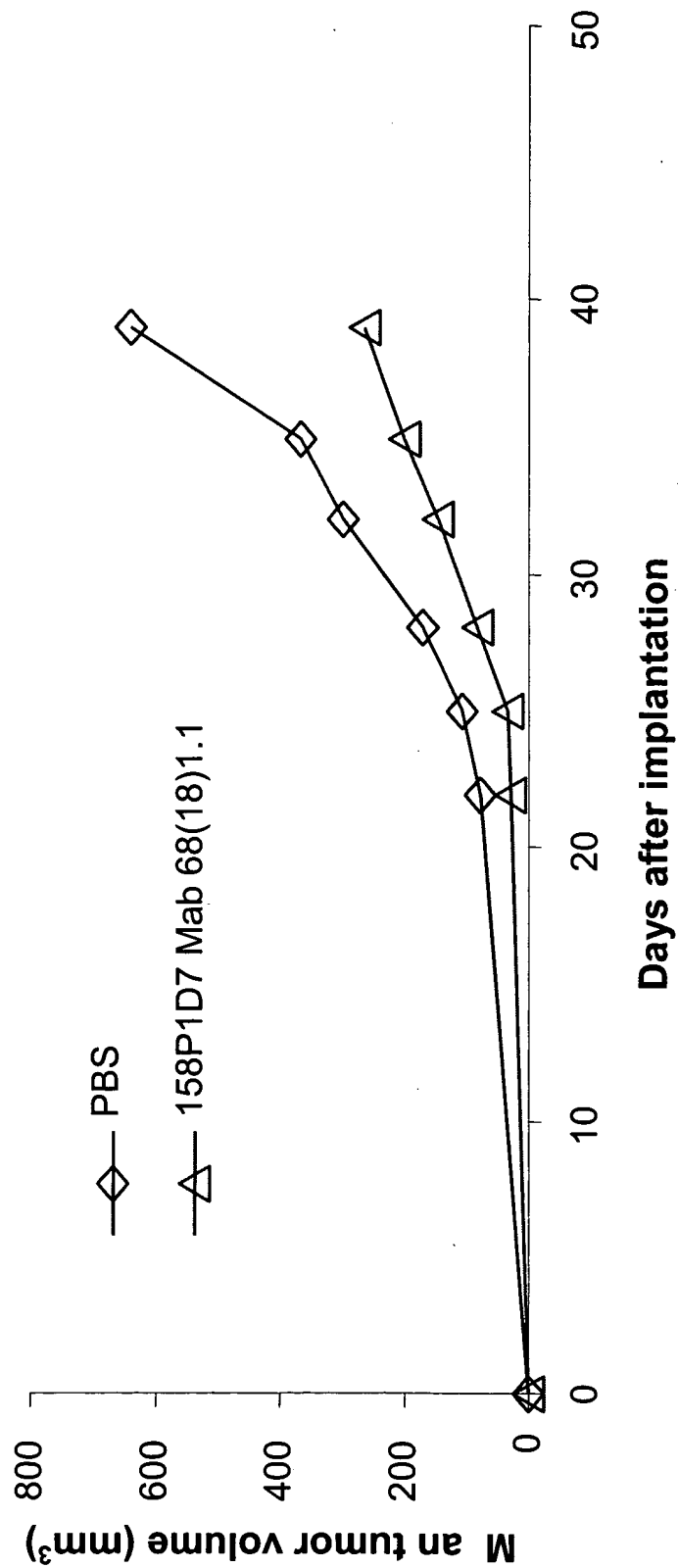


Figure 31 - 158P1D7 MAbs Retard Growth of Human Prostate Cancer Xenografts in Mice

### Patient-derived LAPC9 xenograft

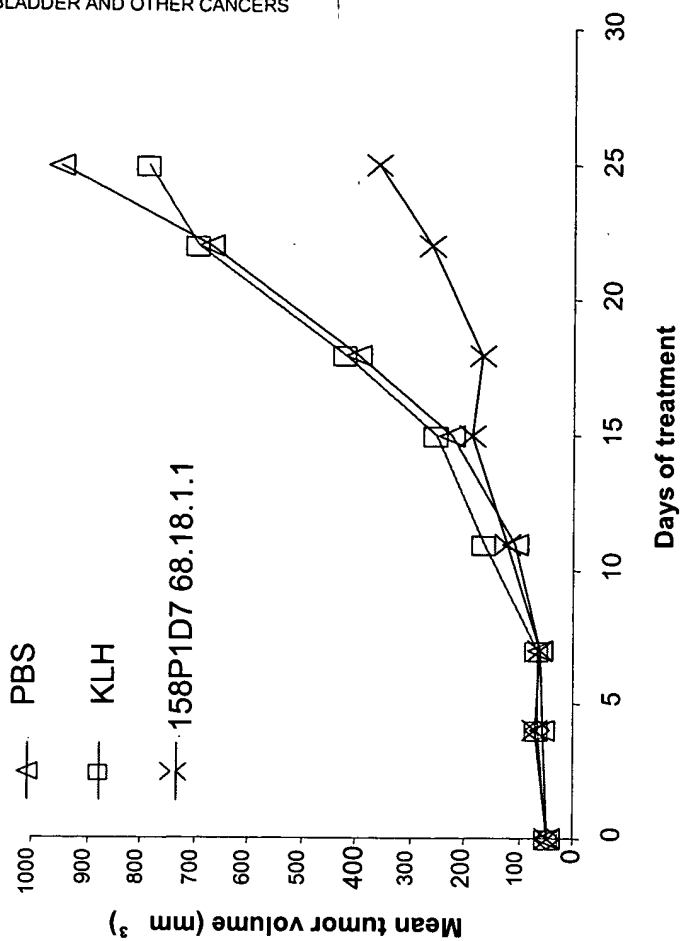
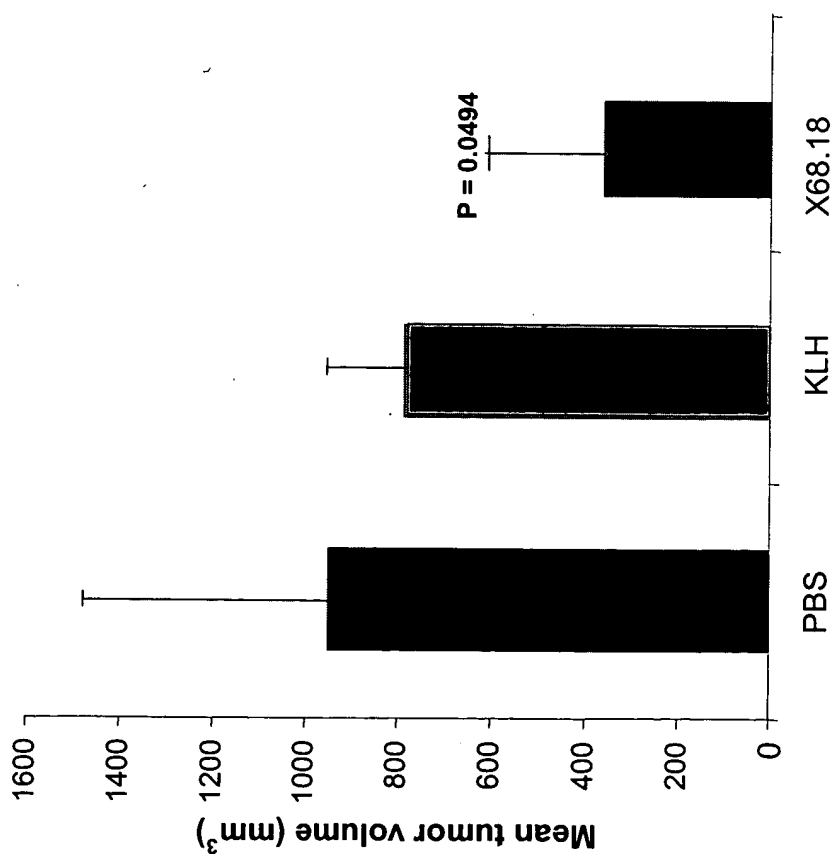


Figure 32: Effect of 158P1D7 on Proliferation of Rat1 cells

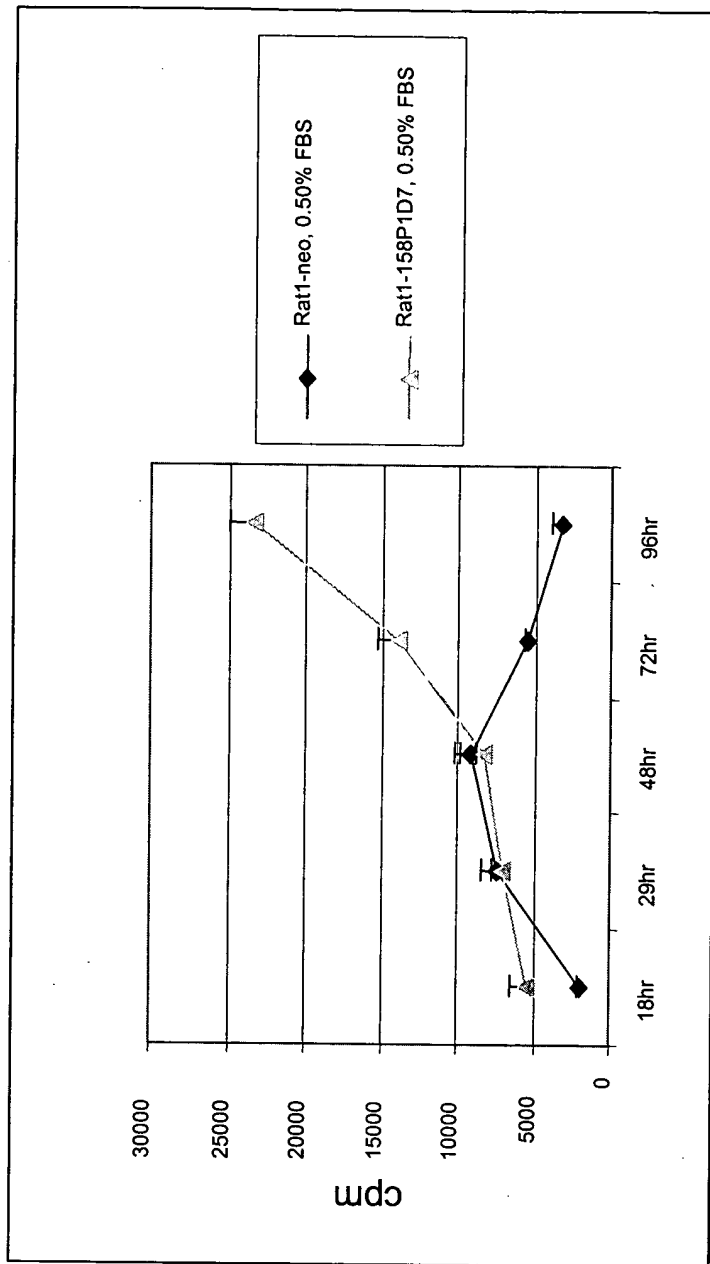


Figure 33: 158P1D7 Enhances Entry Into the S Phase

Cells	Treatment	Percent Cells		
		G1	S	G2
3T3	0.5% FBS	92.7	2.6	2.2
	10% FBS	72.8	11.4	14.7
3T3-neo	0.5% FBS	95.1	1.4	2.3
	10% FBS	59.6	14.1	18.3
3T3-158P1D7	0.5% FBS	90.1	3.3	4.4
	10% FBS	68.4	<b>21.2</b>	1.7

Figure 34A. The cDNA and amino acid sequence of M15/X68(2)18 VH clone #1.

1 Q T A G V R S W P G G A L T E P V H H M  
1 caaactgcaggagtcaggagttggcctggcggcgccctcacagagcctgtccatcacatg  
21 H R L R I L I D R L W C K L G S P A S R  
61 caccgtctcaggattctcattgaccggctatgggtgtaaactgggttcgccagcctccagg  
41 K G S G V A G N D L G R W K H R L Y F S  
121 aaagggctctggggctggggaatgatttggggcgatggaagcacagattatacttcagc  
61 S P I Q T E H Q E G Q F K S Q T F L K N  
181 tctccaatccagactgagcatcaggaaggacaattcaagagccaaactttcttaaaaaat  
81 N S L Q T D D T A R Y Y C A R D E G R G  
241 aacagtctgcaaactgatgacacagccagggtattactgtgccagagatgaagggaggggga  
101 L C L I A G A K G P R S P S P  
301 ctctgtttgattgctggggccaagggaccacgggtcaccgtctcctca

Figure 34B. The cDNA and amino acid sequence of M15/X68(2)18 VL clone #2.

1 D I Q L T Q S P A S L A V S L G Q R A T  
1 gacattcagctgacccagtcctcctgcttccttagctgtatctctggggcagagggccacc  
21 I S Y R A S K S V S T S G Y S Y M H W N  
61 atctcatcacagggccagcaaaagtgtcagtacatctggctatagttatatgcactggaac  
41 Q Q K P G Q P P R L L I Y L V S N L E S  
121 caacagaaaccaggacagccacccagactcctcatctatcttgtatccaacctagaatct  
61 G V P A R F S G S G S G T D F T L N I H  
181 ggggtccctgccagggttcagtggcagtgggctctgggacagacttcaccctcaacatccat  
81 P V E E E D A A T Y Y C Q H I R E L T R  
241 cctgtggaggaggaggatgctgcaacctattactgtcagcacattagggagcttacacgt  
101 S E G G P S W R S N  
301 tcggaggggggaccaagctggagatctaac



**Figure 35A: The amino acid sequence of M15/X68(2)18 VH clone #1.**

1 QTAGVRSWPG GALTEPVHHM HRLRILIDRL WCKLGSPASR KGSGVAGNDL  
51 GRWKHRLYFS SPIQTEHQEG QFKSQTFLEKN NSLQTDDTAR YYCARDEGRG  
101 LCLIAKAKGP RSPSP

**Figure 35B: The amino acid sequence of M15/X68(2)18 VL clone #2.**

1 DIQLTQSPAS LAVSLGQRAT ISYRASKSVS TSGYSYMHWN QQKPGQPPRL  
51 LIYLVSNLES GVPARFSGSG SGTDFTLNIH PVVEEDAATY YCQHIRELTR  
101 SEGGPSWRSN

**Figure 36:** Detection of 158P1D7 protein by immunohistochemistry  
in various cancer patient specimens.

